

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 105953

TO: Karen A Lacourciere

Location: CM-1/11D09/11E12

Art Unit: 1635

Wednesday, October 15, 2003

Case Serial Number: 09/915543

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Lacourciere,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib

From: Sent:

Lacourciere, Karen Tuesday, October 14, 2003 3:13 PM STIC-Biotech/ChemLib

To:

Subject:

Sequence search request 09/915,543

Please perform the following sequence searches for 09/915,543 in the commercial databases, pre-grant pubs and pending files (interference)

- 1) Residues 177-204 of SEQ ID NO:15
- 2) Residues 349-383 of SEQ ID NO:15
- 3) Residues 199-392 of SEQ ID NO:15

Thank-you!

Karen A. Lacourciere Ph.D. CM1 11D09 GAU 1635 (703) 308-7523 mailbox 11E12

> Stickerd Franc Yechnical Info. Speciality STIC/Blotsch CAMB SECENTIAL ROSS-9203

Searcner:
Phone:
Location:
Date Picked Up: 10/15/192
Date Completed 0/103
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 3
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (v	here applic.)
STN:	
DIALOG:	····
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	(1)8
www/Internet:	
Other (specify):	



Comments:

STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

<i>(</i> 0)	umary Results Feedback FUIII	
>	I am an examiner in Workgroup: Example: 1610	•
>	Relevant prior art found, search results used as follows:	
	102 rejection	
	☐ 103 rejection	
	Cited as being of interest.	
	Helped examiner better understand the invention.	
	Helped examiner better understand the state of the art in their technology.	
	Types of relevant prior art found:	
	☐ Foreign Patent(s)	
	☐ Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)	
>	Relevant prior art not found:	
	Results verified the lack of relevant prior art (helped determine patentability).	
	Results were not useful in determining patentability or understanding the invention	

Dropoff or sand completed forms to STIC/Blotseft:Cham Library CMI + Circ. Deak



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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October 15, 2003, 10:27:32; Search time 17.214 Seconds (without alignments) 258.182 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                Run on:
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US-09-915-543-15_COPT_17_204 136 1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 segs, 158726573 residues Searched:

Total number of hits satisfying chosen parameters:

1107863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_19Jun03:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1980.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1981.DAT:* SIDSI_gcgdata_geneseqg-embl_AA1981.DAT:* SIDSI_gcgdata_geneseqg-embl_AA1981.DAT:* SIDSI_gcgdata_geneseqg-embl_AA1981.DAT:* SIDSI_gcgdata_geneseqg-embl_AA1981.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1981.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1980.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1980.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1980.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1980.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA1990.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp-embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp_embl_AA2000.DAT:* SIDSI_gcgdata_geneseq_geneseqp_embl_AA2000.DAT:* SIDSI_gcgdata_g
B 44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		æ				
Result		Query	Query			•
Q	Score	Match	Length	en l	ID	Description
-	136	100.0	1426	23		Human legless homo
7	136	100.0	1435	22	ABB11808	Human BCL9 homolog
3	129	94.9		22	AAO05855	Human polypeptide
4	86	72.1		22	ABB58779	Drosophila melanog
S	86	72.1		23	AAB71228	D. melanogaster lg
9	94	69.1		23	AAU78460	Mouse beta-catenin
7	91	99		23	ABP06595	Human ORFX protein
80	67	49,3		23	AAU78461	Mouse beta-catenin
σ	65	47.8		22	AAO07544	Human polypeptide

Zea mays protein f Zea mays protein f Zea mays protein f Zea mays protein f Drosophila melanog Human polypeptide Novel human diagno Human aminoacyl·tR Human ominoacyl·tR Human aminoacyl·tR Bifidobacterium lo Aspergillus funiga Aspergillus funiga Aspergillus funiga Aspergillus funiga	Arabidopsis thalia	SE	naling pathway; Wnt; Wg; tic; cellular disorder; colon; and neck cancer; brain; thyroid; regeneration; tissue repair.
AAG33446 AAG33445 AAG33444 AABB60387 ABB60387 AAB21574 AAB21574 AAB21574 AAB26271 AAB26271 AAB26489 AAG17973 AAG17973	AAG17973 AAG17973 AAG19363 AAG19313 AAG10431 AAG39799 AAG39799 AAG39799 AAG39799 AAG39799 AAG39799 AAG39799 AAG39799 AAG39798 AAG39798 AAG39798 AAG39798 AAG39798 AAG39798 AAG39798 AAG39799 AAG39799 AAG39799 AAG39799	ALIGNMENTS 1426 AA. Dc19 protein.	signostation states and states and states and states are states are states and states are states are states and states are states ar
		2	ing eas er, 3.
360 448 509 1049 130 365 621 1063 187 1058 498	609 609 609 630 630 11095 11114 11167 11187 11187 1119 1119 1119 1119 1119 1	in the the	n; lgs; Wnt/W eration; tumo r; cancer; br ma; skin canc al. 2001US-091554 2000US-221502 R K. ER E. CH B. S T.
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1111 1111 1111 1111 1111 1111 1111 1111 1111	5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 AAB71229 ID AAB71 XX AC AAB71 XX DT 18-NO XX UX 18-NO	

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; thrombolysis; oncogenesis; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atheroid cell disorder; lymphoid cell disorder; asthma; arthritis; aherosclerosis; coronary heart disease; arterial isochaemia; bone disorder; osteoporasis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; antiasthmatic; antiarthritis; haemostatic; antiarthritis; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (19s) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue respensation and repair. This sequence represents the human legless (19s) protein homologue 19s/bc19 described in the
                                                                        Novel polypeptide useful in therapeutic method for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                          of cell fate such as cell differentiation or cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 136; DB 23; Length 1426; 100.0%; Pred. No. 2.9e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human BCL9 homologue, SEQ ID NO:2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB11808 standard; peptide; 1435 AA.
                                                                                                                                 Example II; Fig 8B; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                WPI; 2002-635689/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1426 AA;
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                                     N-PSDB; AAF88467.
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which con polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence continual therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth activity; have various activities, including cytokine, cell proliferation or cell commondulatory activity; tissue growth activity; inmunomodulatory activities, activities, namboin-related activities; chemotactic or chemokinetic activities; haemostatic, thromboit or from their bological activities, namboit activities or may be not heir bological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietled incoleders (e.g., myelolid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., myelolid or lymphoid cell coronary heart disease, careail schaemia, bone disorders (e.g., ostbma or proliferation and pungal infections in addition to immunomodulatory activities may be used in the treatment of viral, contrained activities and be used in the insurance of viral activities and be used to promote of viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                            Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 136; DB 22; Length 1435; 100.0%; Pred. No. 2.9e-12; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                   Claim 20; Page 256-257; 1963pp; English.
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                                                                                                                                  e.g. arthritis and cancer -
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2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1435 AA;
                      N-PSDB; ABA09052
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemla, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 19747; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%; Score 129; DB 22; Length 140; 92.9%; Pred. No. 2.3e-12; Live 2; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB58779 standard; Protein; 1429 AA.
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                     28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                        26-FEB-2001; 2001WO-US04927
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Matches 26; Conservative
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                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
    Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders -
                                                                                              07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB58779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB58779
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furges. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legless; fruitfly; 1gs; Mnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; breast; had and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3129; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Froesch B, Kramps T, Peter O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.8e-06;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.1%; Score 98; DB 22; Best Local Similarity 57.1%; Pred. No. 2.8e-06; Matches 16; Conservative 9; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                       Wenter JC, Adams M, Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB71228 standard; Protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D. melanogaster lgs protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001; 2001US-0915543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000US-221502P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Basler K, Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-635689/68.
N-PSDB; AAF88466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences (ABL01840-
(ABB57737-ABB72072).
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(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
(KRAM/) KRAMPS T.
                                                                                                                                           WPI; 2001-656860/75
(PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1429 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002086986-A1.
                                                                                                                                                                         N-PSDB; ABL02882
                                                                                                                                                                                                                                                                                                                           interactions -
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1494 AA;

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disorders and cancer caused by over-stimulation of the With pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the brosophila melanogaster (fruitfly) legiess (19s) protein described in the disclosure of the invention.
                                                                                                                                                                                                            This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legiess (19s) protein, a downstream component of the Wnr/Wingless (Wnr/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tunnours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
Novel polypeptide useful in therapeutic method for treating disorders of cell fate such as cell differentiation or cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and DNA encoding the protein. The protein and encoding DNA rate applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a beta-catenin nuclear localised protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.1%; Score 98; DB 23; Length 14
Best Local Similarity 57.1%; Pred. No. 2.9e-06;
Matches 16; Conservative 9; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; EST; expressed seguence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::||||::||| ||:|| || :|| 345
318 IFVFSTQLANKGAESVLSGQFQTIIAYH 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 81-88; 113pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU78460 standard; Protein; 1494 AA.
                                                                                                                                   Example II; Fig 2; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-2000; 2000JP-0287876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-330014/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1464 AA;
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABMIST55 to ABMIST55 encode the human ORFX proteins given in ABB00010 to ABPIL500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynuclectide squences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the remaind of syndrome associated with ORFX-associated disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, insendringe, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic tumoslantation, artious immune disciencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthitis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bene degenerative disorders, or periodontal disease, and for gut
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                                                                                                                                                                                                                                                                                                                                                                                                        Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; behign tumour; hemomrhinage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertensison; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                           6
  Length 1494;
                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorders and autoimmune disorders
69.1%; Score 94; DB 23; 60.7%; Pred. No. 1.3e-05; Live 8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                 Human ORFX protein sequence SEQ ID NO:13172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID 13172; 1037pp; English.
                                                                                                                          238 VYVETTHLANTAAEAVLQGRAESILAYH 265
                                                                                      1 VYVFSTEMANKAAEAVLKGOVETIVSFH 28
                                                                                                                                                                                                                                     ABP06595 standard; Protein; 114 AA
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                                                                                                                                                                                                                                                                                                                         25-JUN-2002 (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Leach MD;
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                  Local Similarity
es 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myasthenia gravis.
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    Query Match
                                           Matches
                                                                                                                                                                                                RESULT 7
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AA007544 standard; Protein; 113 AA.
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                                  AAO07544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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  AAO07544
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protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytchine damage.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein #2.
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                                                                                                       Length 114;
                                                                                                    Query Match 66.9%; Score 91; DB 23; Length 11 Best Local Similarity 57.1%; Pred. No. 1.7e-06; Matches 16; Conservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                     Mouse; beta-catenin nuclear localised protein; cancer; gene therapy; EST; expressed sequence tag.
                                                                                                                                                                                                                                                                                                Mouse beta-catenin nuclear localised protein #2.
                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                              1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 91-92; 113pp; Japanese.
                                                                                                                                                                                                                              AAU78461 standard; Protein; 320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 MANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-2000; 2000JP-0287876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3est_Local Similarity 57.19
4atches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-330014/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 AA;
                                                                                Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                            WO200224738-A1.
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akiyama T,
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                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                  Human polypeptide SEQ ID NO 21436.
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990S-0145085 990S-0145087 990S-0145087 990S-0145192 990S-0145145 990S-0145218 990S-0145218 990S-0145913 990S-0145913 990S-0146388 990S-0146388 990S-0146388 990S-0146388 990S-0147302 990S-0147303 990S-0147403 990S-01474103 990S-01474103 990S-01474103 990S-01474103 990S-01474103 990S-01474103 9905 - 0140353 9905 - 0140635 9905 - 0140635 9905 - 0140691 9905 - 0141287 9905 - 0141287 9905 - 0141287 9905 - 0141283 9905 - 014230 9905 - 014230 9905 - 014352 9905 - 014433 9905 - 0144836 990S-0149722. 990S-0149723. 990S-0149929. 990S-0149902. 99US-0149930. 99US-0148684. 99US-0149368. 99US-0149175. 99US-0149426. 990S-0150884. 990S-0151065. 990S-0151066. 990S-0151080.

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990'S-0156596.
990'S-0157117.
990'S-0157753.
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Best Local Similarity 50.0%
Matches 12; Conservative
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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99US-0161993.
99US-0162142.
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99US-0154779.
99US-0155139.
99US-0155486.
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                        24-SEP-1999;
28-SEP-1999;
04-OCT-1999;
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23-MAR-1999; 25-MAR-1999; 25-MAR-1999; 26-MAR-1999; 26-MAR-1999; 21-APR-1999; 21-APR-1999; 23-APR-1999; 23-APR-1999; 24-MAY-1999; 24-MAY-1999; 25-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 26-MAY-1999; 27-MAY-1999; 28-MAY-1999; 28-MAY-1999; 39-MAY-1999;	01-JUL 01-JUL 02-JUL 06-JUL 08-JUL 09-JUL 12-JUL 13-JUL

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Matches
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Pred. No. 14;
2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 7953.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD, Myers EW;
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                                                                                                                                                                                                                                      4 FSTEMANKAAEAVLKGQVETIVSF 27
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ilarity 50.0%;
Conservative
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11-JUL-2000; 2000US-0614150.
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99US-0157753.
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Best Local Similarity
Matches 12; Conserv
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21-0CT-15
21-0CT-15
21-0CT-19
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21-0CT-1
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabletic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antimagal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                    is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                         Disclosure; SEQ ID NO 7953; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%; Score 51; DB 22; Length 1049; 40.7%; Pred. No. 49; Live 5; Mismatches 11; Indels
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                                                                            interactions -
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isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anamia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                   130 AA;
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             a food supplement. (II) and its binding partners are useful in mice and a food supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
quantitating a polypeptide in tissue, as molecular weight markers and as
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                                                                                                                                                                                                                                                                                                                                               36.8%; Score 50; DB 22; Length 365; 29.6%; Pred. No. 20;
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8; Mismatches
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Matches 8; Conservative
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October 15, 2003, 10:27:32; Search time 5.66537 Seconds (without alignments) 209.113 Million cell updates/sec
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4: cgn2_6/ptodata1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/laa/pcTUS_COMB.pep:*
GenCore version 5.1.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                           US-09-915-543-15_COPY_177_204
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                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                      Perfect score: 136
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                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 3	Appli	Appli	Appli	App1	~	-	-			, Appl	Appl ,	App1				_	, Appl	, Appl			29737, A	219, App	Appli	Appl ,	Appli	Appl	Appli
_ ;	3,	'n	ć	37,	93,	103	93,	93,	93,	93,	93,	63	63	29,	93,	83	88	88	103,	210,	29	21	8	Π	8	20	ń
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-09-080-983-3	US-08-080-080-2	US-09-447-453-2	US-09-091-725-37	US-08-486-099-93	US-08-360-107A-103	US-08-484-223B-93	US-08-919-597-93	US-08-475-668A-93	US-08-485-551A-93	US-08-471-913A-93	US-08-485-264A-93	US-08-474-349A-93	US-08-255-208A-29	US-08-470-896-93	US-08-485-546A-93	US-08-224-657-88	US-09-354-138-88	US-09-732-210-103	US-09-732-210-210	US-09-252-991A-29737	US-09-634-238-219	US-09-934-901-8	US-09-627-376-11	US-07-998-289B-8	US-09-775-932-20	US-08-844-085-2
DB	3	٣	m	4	m	m	۳	m	3	m	m	m	7	4	4	4	٦	4	4	4	4	4	4	4	m	4	Н
% Query Match Length DB	2639	718	718	145	438	438	438	438	438	438	438	438	438	438	438	438	662	662	154	154	188	300	358	541	1820	111	678
% Query Match	34.6	32.4	32.4	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.5	30.5
Score	47	44	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	42	42	42	42	42	42	42	41.5	41.5
Result No.	1	7	m	4	Ŋ	9	7	6 0	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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-Juence 5, Appli
Sequence 43, Appli
Sequence 43
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Sequence 5449, Ap
Sequence 3670, Ap
Sequence 1, Appli
Sequence 6, Appli
Sequence 6500, Ap
Sequence 6689, Ap
Sequence 5806, Ap
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Sequence 43, Appl
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Sequence 43, Appl
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                                                             Sequence
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhu, Hai Ying
APPLICANT: Ling, Kai-Shu
APPLICANT: Ling, Kai-Shu
APPLICANT: Ling, Kai-Shu
APPLICANT: Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS TYPE 2 PROTEINS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.6%; Score 47; DB 3; Length 2639; 33.3%; Pred. No. 1.3e+02; Live 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                 US-08-453-952-5
US-08-484-1588-43
US-08-484-1588-43
US-08-484-1588-43
US-08-48-1508-43
US-08-48-1508-43
US-08-107-5328-5449
US-09-107-5328-5449
US-09-107-5328-6500
US-09-107-5328-6689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERCE/DOCKET NUMBER: 19603/1631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,194
FILING DATE: 20-MAX-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3, Application US/09080983; Patent No. 6197948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2639 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
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MEDIUM TYPE: Floppy
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U.S.A.
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Best Local Similarity
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New 3
COUNTRY: U.:
ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-09-080-983-3
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US-09-080-983-3
Matches
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 718 amino acids
                                                                                                                         IBM Compatible
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-09-447-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                         COMPUTER: IBM CONTOURNEY: OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United ZIP: 20006-1888
  Palo Alto
                                         USA
                                                                                                                                                                                                                             FILING DATE
                                                               94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-091-725-37
                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Mitofusin Genes and their
TITLE OF INVENTION: Uses
OF INVENTION: Uses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             TITLE OF INVENTION: Mitofusin Genes and their TITLE OF INVENTION: Uses
TORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BOAIGEVIC & Reed, LLP
TREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SISTEM: DOS
SOFTWARE: FASLEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
                     2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 YCFEELTEMTORVGRCVLSDOIKTLI 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUN-63P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,961
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09447453; Sequence 2, Application US/09447453; Patent No. 6284507; GENERAL INFORMATION:
APPLICANT: Hales, Karamaticant APPLICANT: Hales & Karamaticant APPLICANT: Hales
                                                                                                                                         Sequence 2, Application US/09090808
Patent No. 6127159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /AGENT INFO......
Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: SUR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                      APPLICANT: Fuller, Margaret APPLICANT: Hales, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 718 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-090-808-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   94301
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                                                                                                                       US-09-090-808-2
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                                                                                                    RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
32.4%; Score 44; DB 3; Length 718;
Best Local Similarity 34.6%; Pred. No. 79;
Matches 9; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster 11p
STREET: 2000 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 YCFEELTEMTQRVGRCVLSDQIKTLI 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
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                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 06/-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36/677
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                         SUN-63P
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 37, Application US/09091725
; Patent No. 6329141
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Wed Oct 15 11:40:23 2003

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APPLICANT: Harney, Shawn O.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: WEMBRAME FUSION ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        Gaps
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31.6%; Score 43; DB 3; Length 438;
Best Local Similarity 36.4%; Pred. No. 63;
Matches 8; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                   Query Match 31.6%; Score 43; DB 4; Length 145; Best Local Similarity 43.8%; Pred. No. 16; Matches 14; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: US-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                     5 STEMANKAA-EAVLKG-----QVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                   15 SADVKAKAAKKAALKGTQSTSTRKVRTSVSFH 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7872-031
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 93, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
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TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787;
TELECOMMUNICATION INFORMATION:
TELEBHOME: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
NAME: E. Victor Donahue
REGISTRATION NUMBER: 35,49
INFORMATION FOR SEQ ID NO: 37,
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                        TOPOLOGY: linear;
MOLECULE TYPE: protein US-09-091-725-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Pred. No. 63;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTER: USA
COUNTER TEADABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIAL PC-DOS/MS-DOS
SOFTWARE: PATENTIA RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/360,107A FILING DATE: 20-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7872-013
                                  ; Sequence 103, Application US/08360107A; Patent No. 6017536
                                                                                                                                                        APPLICANT: Barney, Shawn O. APPLICANT: Lambert, Dennis M. APPLICANT: Lambert, Dephen R. APPLICANT: Langlois, Alphonse J. TITLE OF INVENTION: METHODS AND CONTINE OF INVENTION: TRANSMISSION TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 STEMANKAAEAVLKGQVETIVS 26
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; Patent No. 6020459
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Lambert, Dennis M.
Petteway, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9990
TELERAX: (212) 869-9741/8864
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
                                                                             GENERAL INFORMATION:
APPLICANT: BOLOGNESI, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORIEY/AGENT INFORMATION:
NAME: COLUZZI, LAULA A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.6%;
36.4%;
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Best Local Similarity 36.4;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-360-107A-103
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & I
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                              New York
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RESULT 6
US-08-360-107A-103
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US-08-484-223B-93
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBERANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
Langlois, Alphonse J. INPERTION OF COMPOSITIONS FOR INHIBITION OF WEMPINE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B FILING DATE: US/05/484,223B CIASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 93, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | | | : : | | : : 41 SLEQSNKAIEEIREATQETVIA 62
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                                                                       TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741/BBE TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 438 amino acids TYPE: amino acid
                                                                                                   245
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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US-08-919-597-93
     APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Lannbert, Dennis M.
APPLICANT: Lannbert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.6%; Score 43; DB 3; Length 438; illarity 36.4%; Pred. No. 63; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.30 CURREMY APPLICATION DAYA: APPLICATION NDAYA: FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
APPLICATION: 424
               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/919,597
                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7672-020
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 STEMANKAAEAVLKGQVETIVS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 93, Application US/08475668A; Patent No. 6060065
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE FINFORMATION FOR SEQ 1D NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKEY NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-919-597-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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ZIP: 10036-2711
                                                                                                                CLASSIFICATION:
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APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Stephen R.
APPLICANT: Langlois, Alphones J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
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Pred. No. 63;
6; Mismatches 8; Indels
                                                                                                                                       Query Match 31.6%; Score 43; DB 3; Length 438; Best Local Similarity 36.4%; Pred. No. 63; Matches 8; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
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...ьек: US/08/485,551A
07-JUN-1995
тиг. 435
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41 SLEQSNKAIEEIREATQETVIA 62
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COULZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-0
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
                                                                                                                                                                                                                           5 STEMANKAAEAVLKGQVETIVS 26
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
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36.4%;
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LENGTH: 438 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 36.4%
Local Similarity 36.4%
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-485-551A-93
                                                            TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
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New York
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                                                                                                       US-08-475-668A-93
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STATE:
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APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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SYSTEM: PC-DOS/MS-DOS
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                                        ; Sequence 93, Application US/08471913A; Patent No. 6093794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                           Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
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ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
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Matches 8; Conserv
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                                                                                          GENERAL INFORMATION:
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RESULT 11
US-08-471-913A-93
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STATE:
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APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: VIRUS TRANSMISSION
TITLE OF INVENTION: VIRUS TRANSMISSION
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.6%; Score 43; DB 3; Length 438; Best Local Similarity 36.4%; Pred. No. 63; Matches 8; Indels Matches 8; Indels
                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                             E: Pennie & Edmonds LLP
1155 Avenue of the Americas
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 STEMANKAAEAVLKGQVETIVS 26
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41 SLEQSNKAIEEIREATQETVIA 62
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TELEFAX: (222) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennie & Edmonds
                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 438 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : MOLECULE TYPE: protein US-08-485-264A-93
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CORRESPONDENCE ADDRESS:
                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                     New York
: USA
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                                                                                                               New York
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                                                                  ADDRESSEE:
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                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Balognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pertteway Jr., Stephen R.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 111
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F: 1155 Avenue of the Americas
New York
: New York
YY: USA
                                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,208A
FILLING DATE: 07-JUN-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US/08/474,349A PILLING DATE: 07-JUN-1995
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 STEMANKAAEAVLKGQVETIVS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 SLEQSNKAIEEIREATQETVIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHRRACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: COIUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                              INFORMATION:
                                                                                                                                                                                                                                                                           LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-474-349A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                    FILING DATE: 07
CLASSIFICATION:
ATTORNEY/AGENT INE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-255-208A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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US-08-255-208A-29

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                                                                                                                                                                                                                                                           APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Midd, Carl I.
APPLICANT: Midd, Carl I.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphones J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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               31.6%; Score 43; DB 4; Length 438; 36.4%; Pred. No. 63; Live 6; Mismatches 8; Indels
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63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CURSIFICATION: 435
MEDANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%; Score 43; DB 36.4%; Pred. No. 63; tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 790-9090
TELERX: (512) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                     41 SLEQSNKAIEEIREATQETVIA 62
                                                                                             5 STEMANKAAEAVLKGQVETIVS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 STEMANKAAEAVLKGQVETIVS 26
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41 SLEQSNKAIEEIREATQETVIA 62
                                                                                                                                                                                      RESULT 15
US-08-470-896-93
; Sequence 93, Application US/08470896
; Patent No. 6479055
438 amino acids
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Best Local Similarity 36.4
Matches 8; Conservative
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: MOLECULE TYPE: protein
US-08-470-896-93
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Search completed: October 15, 2003, 10:31:58 Job time : 6,66537 secs

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October 15, 2003, 10:32:06; Search time 11.8755 Seconds (without alignments) 379.908 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_MEW_UBB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_MEW_UBB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600653 seqs, 161128416 residues
                                                                                                                                                                                                                                                                                                                                                                       US-09-915-543-15_COPY_17_204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 3547, Ap	Sequence 8547, Ap	Sequence 6, Appli	Sequence 8, Appli	Sequence 10, Appl	Sequence 10721, A	Sequence 92, Appl	Sequence 9002, Ap	Sequence 10457, A	Sequence 2, Appli	Sequence 5144, Ap	Sequence 212, App
ΩI	US-10-322-579-3	US-10-322-579-15	US-10-322-579-2	US-10-128-714-3547	US-10-128-714-8547	US-10-008-355-6	US-10-167-547C-8	US-10-167-547C-10	US-10-156-761-10721	US-10-342-224-92	US-10-156-761-9002	US-09-815-242-10457	US-10-117-846-2	US-09-764-891-5144	US-10-306-762-212
DB	15	15	15	15	15	14	12	12	15	12	15	6	14	11	12
% Query Match Length DB	28	1426	28	984	1058	732	471	507	747	170	171	484	718	80	315
% Query Match	100.0	100.0	72.1	36.0	36.0	34.6	33.8	33.1	33,1	32.7	32.4	32.4	32.4	31.6	31.6
Score	136	136	86	49	49	47	46	45	45	44.5	44	44	44	43	43
Result No.	1	7	ťΩ	4	īΟ	9	7	8	0	10	11	12	13	14	15

sequence 7819, Ap Sequence 141, App Sequence 8136, App Sequence 8136, App Sequence 8136, App Sequence 18, Appli Sequence 18, Appli Sequence 142, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1197, App Sequence 1197, App Sequence 1197, App Sequence 128, Appli Sequence 1197, App Sequence 1197, App Sequence 1197, App Sequence 1197, App Sequence 10, Appli Sequence 5086, Appli Sequence 5086, Appli Sequence 5086, Appli Sequence 11, Appli Appli Sequence 11, Appli Appli Sequence 11, Appli Appli Sequence 11, Appli Appl	30 30 27
12 US-10-032-585-7819 11 US-99-951-051A-141 15 US-10-097-111-304 15 US-10-156-761-9336 16 US-09-934-901-8 17 US-09-934-901-8 18 US-10-156-761-9336 19 US-09-934-901-8 10 US-09-934-901-8 12 US-10-320-924-8 12 US-10-320-924-8 14 US-10-320-924-8 15 US-09-932-227-42 17 US-09-932-227-42 18 US-08-781-986A-5245 19 US-09-815-242-1036 10 US-09-910-186A-12 11 US-09-910-186A-12 12 US-09-815-242-1036 13 US-09-815-242-1036 14 US-09-815-242-1036 16 US-09-815-242-1036 17 US-09-815-242-1036 18 US-08-136-242-1036 19 US-09-815-242-1036 19 US-09-815-242-296 11 US-09-815-242-296 12 US-09-815-242-296 13 US-09-815-242-296 14 US-10-055-664-1	US-09-741-669-39 US-10-234-432-3 US-10-234-432-5 US-10-234-432-5
623 6623 6623 6623 3326 3326 3358 3358 3360 340 370 370 370 370 370 370 370 370 370 37	693 727 727
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ALIGNMENTS

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Sequence 3, Application US/1032579
; Bedulence 3, Application US/1032579
; Publication No. US20030114413A1
; GENERAL INFORMATION.
APPLICANT: BASLER, Konrad
APPLICANT: BROWNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, BARDARA
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH:
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
TITLE OF INVENTION: UNUBER: US/10/322,579
CURRENT APPLICATION NUMBER: US/10/322,579
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 28
LENGTH: 28
LENGTH: 28
LENGTH: 28
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Human lgs/bcl9
US-10-322-579-3
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Best Local Similarity
Matches 28; Conserv
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us-10-322-579-15 RESULT 2

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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Hu, Wenqi
APPLICANT: Talahoff, Daniel
APPLICANT: Talahoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Expandio, Carlos
APPLICANT: Expandio, Carlos
APPLICANT: Emeleux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Morber: US/10/128,714
CURRENT PILING DATE: 2001-04-23
FRIOR PAPLICATION NUMBER: US 60/285,697
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin Version 3.1
SEQ ID NO 3547
TENDER DATE: DATE ON 0.3547
TENDER DATE ON 0.3547
TENDER DATE ON 0.3547
TENDER DATE ON 0.3547
TENDER DATE ON 0.3547
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Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Eamudo, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%; Score 49; DB
52.6%; Pred. No. 46;
Live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VFSTEMANKAAEAVLKGQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Aspergillus fumigatus US-10-128-714-8547
                       Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 52.6'
Matches 10; Conservative
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Sequence 15, Application US/1032579
Publication No. US2003011441341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BASIER, Konrad
APPLICANT: BRUNNER, Erich
APPLICANT: FROESCH, Barbara
APPLICANT: RAMPS, Thomas
APPLICANT: REAMPS, Thomas
TITLE OF INVENTION: ESSEWITAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: BSSEWITAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE REFERENCE: Q60361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOSTWARE: PATENTIN VERSION 3.1
SEQ ID NO 15
LENGTH: 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10322579
Publication No. US20030114413A1
GENERAL INFORMATION:
APPLICANT: BASLER, Konrad
APPLICANT: BRUNNER, Erich
APPLICANT: KRAMPS, Thomas
APPLICANT: KRAMPS, Thomas
APPLICANT: PETER, Oliver
ITTLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 100.0%; Score 136; DB 15; Local Similarity 100.0%; Pred. No. 9.4e-13; Nes 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 060361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEG ID NO 2
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
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US-10-128-714-3547
; Sequence 3547, Application US/10128714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human 1gs/bc19
US-10-322-579-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Drosophila lgs
US-10-322-579-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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US-10-167-547C-10

Sequence 10, Application US/10167547C

Publication No. US20330170653A1

Publication No. US20330170653A1

APPLICANT: E.I. du Pont de Nemours and Company

APPLICANT: Damude, Howard G.

TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gam;

FILE REFERENCE: CL1804 US NA

CURRENT APPLICATION NUMBER: US/10/167,547C

PRIOR PELING DATE: 2003-03-17

PRIOR FILING DATE: 2001-06-08
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US-10-342-224-92
; Sequence 92, Application US/10342224
; Publication No. US20030162294A1
; GENERAL INFORMATION:
; APPLICANT: Nathalie Verbruggen
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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33.1%; Score 45; DB 12; Length 507;
Best Local Similarity 37.5%; Pred. No. 90;
Matches 9; Conservative 5; Mismatches 10; Indels
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SAKKI, YOSHIUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PELING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10721, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEBA, HARUO
APPLICANT: ISHIRMA, JUN
APPLICANT: SHIRMA, JUNSHI
APPLICANT: SHIRMA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 FSTRLANNLENLIVKEGPDTIAAF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FSTEMANKAAEAVLKGQVETIVSF 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.1%;
Best Local Similarity 39.1%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 10
LENGTH: 507
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SEQ ID NO 10721
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                           : ORGANISM: Alstroemeria
US-10-167-547C-10
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Publication No. US20030170653A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT FILING DATE: 2003-03-17
PRIOR FILLGATION NUMBER: 60/297198
PRIOR FILLIG DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
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; Bublication No. US2002016475941
; GENERAL INNORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potemma, Jan S
; APPLICANT: Banbula, Agnieszka
; TITLE OFF INVENTION: Dipeptidylpeptidases And Methods Of Use
; FILE REFERENCE: 235, 00444011
; CURRENT APPLICATION NUMBER: US/10/008,355
; PRIOR APPLICATION NUMBER: US 60/246,827
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 732
                    Score 49; DB 15; Length 1058;
Pred. No. 50;
4; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 732;
67;
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41.7%; Pred. No. 57;
tive 4; Mismatches
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517 VALYDTNWAQEKAEKILAGKLST 539
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                                                                                                                                        ; TYPE: PRT
; ORGANISM: Shewanella putrefaciens
US-10-008-355-6
                                                                                                            3 VESTEMANKAAEAVLKGQV 21
                  Query Match 36.0%;
Best Local Similarity 52.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Office 07 SEQ ID NO 8
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Best Local Similarity 41.7
Matches 10; Conservative
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US-10-167-547C-8
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Best Local Similarity
Matches 9; Conserva
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US-10-008-355-6
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US-10-117-846-2
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                                                                                                                                                                                                                                                                                                                    Pred. No. 29;
0; Mismatches
FILE REFERENCE: CNN-012US
CURRENT APPLICATION NUMBER: US/10/342,224
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US/09/762,154
PRIOR FILING DATE: 2002-02-02
PRIOR FILING DATE: 1998-04
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
LENGTH: 170
                                                                                                                                                                                                                                                                                            Query Match 32.7%; Score 44.5; Best Local Similarity 52.0%; Pred. No. 29; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISHIKAWA, UUN
APPLICANT: BARIKAWA, UUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASHIRA
TITLE REPERBANCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILIKG DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-05-30
SEQ ID NOS: 15109
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Fatent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                6 TEMANKAAEAVL----KGQVETIV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9002, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9002
                                                                                                                                                                                                                                    ; ORGANISM: Arabidopsis thaliana
US-10-342-224-92
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35.7%;
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Xu, H. Howard
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Trawick, John D.
Carr, Grant J.
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Best Local Similarity
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US-09-815-242-10457
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                                                                                                                                                                                                                      TYPE: PRT
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APPLICANT: Hales, Karen G.
APPLICANT: Hales, Karen G.
FAPPLICANT: Sancel, Ansgar H.
TITLE OF INVENTION: Mitofusins, Fzo Homologs and Functional
TITLE OF INVENTION: Derivatives Thereof
FILE REFERENCE: STAN 063CIP3
CURRENT PAPLICATION NUMBER: US/10/117,846
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/413,285
PRIOR APPLICATION NUMBER: PCT/US00/27871
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1000-10-06
PRIOR FILING DATE: 2000-10-06
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 718
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes; FILE PREFERENCE: ELITRA.011A; CURRENT APPLICATION NUMBER: US/09/815,242; CURRENT PILLING DATE: 2001-03-21; PRIOR APPLICATION NUMBER: 60/191,078; PRIOR PRIOR FILING DATE: 2000-03-21; PRIOR PRIOR FILING DATE: 2000-05-23; PRIOR FILING DATE: 2000-05-23; PRIOR PILING DATE: 2000-05-26; PRIOR APPLICATION NUMBER: 60/207,727; PRIOR APPLICATION NUMBER: 60/207,727; PRIOR APPLICATION NUMBER: 60/25-36; PRIOR FILING DATE: 2000-11-27; PRIOR APPLICATION NUMBER: 60/25-36; PRIOR FILING DATE: 2000-11-27; PRIOR PRIING DATE: 2000-11-27; PRIOR PRIING DATE: 2000-11-27; PRIOR PRIING DATE: 2000-11-27; PRIOR FILING DATE: 2000-11-27; PRIOR FILING DATE: 2000-11-27; PRIOR FILING DATE: 2000-11-27; PRIOR FILING DATE: 2000-11-37; PRIOR FILING DATE: 2000-10-216; NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 484;
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30.0%; Pred. No. 1.2e+02;
tive 7; Mismatches 7; Indels
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; Sequence 5144, Application US/09764891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10117846
Publication No. US20020168673A1
GENERAL INFORMATION:
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52 LLRKSVSVIIKGTIKTIIGF 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.45
Best Local Similarity 30.05
Matches 6; Conservative
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US-09-815-242-10457
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.;
ITILE OF INVENTION: Uncleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5144
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-5144
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US-10-306-762-212

Sequence 212, Application US/10306762

Sequence 212, Application No. US20030187220A1

Sequence 212, Application No. US20030187220A1

GENERAL INFORMATION:
APPLICANT: Park, Frances

APPLICANT: Buchanan, Sean Grant
APPLICANT: Buchanan, Sean Grant
TITLE OF INVENTION: Wichael

TITLE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
FILE REFERENCE: 52498-20011.00

CURRENT APPLICATION NUMBER: US/10/306,762

CURRENT APPLICATION NUMBER: US 60/334,132

PRIOR APPLICATION NUMBER: US 60/334,132

PRIOR APPLICATION NUMBER: US 60/334,132

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
31.6%; Score 43; DB 12; Length 315;
Best Local Similarity 39.1%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.6%; Score 43; DB 11; Length 80; Best Local Similarity 34.8%; Pred. No. 20; Matches 8; Indels Matches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VYVFSTEMANKAAEAVLKGQVET 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 MHIFSSEYANKPVTAISAMHMQT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ 1D NO 212

: LENGTH: 315

: TYPE: PRT

: ORGANISM: A. tumefaciens (15888840)

US-10-306-762-212
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1;

Gaps

5;

Search completed: October 15, 2003, 10:50:57 Job time: 13.8755 secs

6 TEMANKAAEAVLKGQVETIVSFH 28 29 TEMI - VADAIIHGQREKLLGYH 49

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 15, 2003, 10:27:32; Search time 6.64591 Seconds (without alignments) 405.170 Million cell updates/sec Run on:

US-09-915-543-15_COPY_17_204 136 1 VYVFSTEMANKAABAVLKGQVETIVSFH 28

Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5

Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_76:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	porphobilingen sv	- 0		protein F17L21.2	probable response	SqaT protein VCA02	probable D-2-hydro	dihydroxyacetone k	hypothetical prote	prolidase (Xaa-Pro	probable bacterion	hypothetical prote		in	probable aminotran	hypothetical prote	probable acetyl-Co	class II histocomp	qlutaconate CoA-tr	cellulase (EC 3.2.	ase	DIC	٠.			Q	hypothetical profe		Ω.
	ID	140812	T27465	G97070	D86398	F71315	D82484	C81380	E84074	T01822	F90179	AD0623	T29695	808500	C69962	E95887	F72308	855089	S04363	A99261	S54744	S39962	H72478	B96495	н96762	D90907	F85710	T43131	T14645	C64445
	DB	. 0	7	7	7	~	C1	~	7	~	~	7	~				7	7	~	7	CI	~	7	~	7	7	7	~	7	7
	Length	205	634	243	210	458	586	311	330	319	352	662	586	330	363	461	1289	2123	256	268	504	505	131	451	555	48	20	126	265	318
œ	Query	44.1	0	7	ဖ	Ġ	9	ഗ	35.3	4	34.6	34.6	4	33.8	33.8	α	33.8	33.8	33.5	33.5	33.5	33.5	33.1	•	33.1	32.7	32.7	32.4	32.4	32.4
	Score	09	52	51	49	49	4	48.5	48	47	47	7	46.5	46	46	46	46	46	45.5	S	45.5	•	45	45	45	44.5	44.5	44	44	44
	Result No.	г	7	m	4	5	9	7	æ	on.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical protein Y87G2A.m - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T27465
R;White, S.
Submitted to the EMBL Data Library, September 1999
A;Reference number: Z20371
A;Accession: T27465
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Molecule type: DMA
A;Residues: 1-634 < WIL>
A;Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54487.1; CESP:Y87G2A.m
A;Experimental source: clone Y87G2A
A;Gene: CESP:X87G2A.m
A;Introns: 74/1; 270/1

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Gaps

; 0

Query Match
40.4%; Score 55; DB 2; Length 634;
Best Local Similarity 44.4%; Pred. No. 4.2;
Matches 12; Conservative 2; Mismatches 13; Indels

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Gaps

; 0

Length 205; Indels

DB 2;

Query Match
44.1%; Score 60; DB 2,
Best Local Similarity 46.2%; Pred. No. 0.23;
Matches 12; Conservative 5; Mismatches

2 YVFSTEMANKAAEAVLKGQVETIVSF 27

οğ qq RESULT 2

phosphate carrier probable transposo acriflavin resista probable bnArpanto probable transport hypothetical brote hypothetical prote probable 1,2-diacy vibriolysin (EC 3. probable DNA ligas valine-tRNA ligas polyketide synthas hypothetical prote 6,7-dimethyl-8-rib hypothetical prote 6,7-dimethyl-8-rib	RESULT 1 140812 Porphobilinogen synthase (EC 4.2.1.24) - Clostridium josui (fragment) Porphobilinogen synthase (EC 4.2.1.24) - Clostridium josui (fragment) N.Alternate names: delta-aminolevulinic acid dehydratase C.Species: Clostridium josui C.Species: clostridium josui C.Species: lof-aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999 C.Accession: 140812 R.Pujino, E.; Rujino, T.; Karita, S.; Sakka, K.; Ohmiya, K. Bacteriol. 177, 5169-5175, 1995 A.; Reference number: A57344; MUID:95394829; PMID:7665501 A.; Reference number: A57344; MUID:95394829; PMID:7665501 A.; Residues: 1-205 <
119105 A88016 A74455 A74498 A31051 A81116 D65230 D65230 D65230 D7509 JC5756 JC5756 JC57709 JC57709 JC7709 JC7709 A813133	ALIGN 1.24) - ulinic - ision 16 S.; Sak 5 f some 9 95394829 from GB from GB
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4 4 4 4 4 4 4 4 4 4 6 7 7 7 7 7 8 8 8 8 8 8 8 8 7 8 7 8 8 8 8 8 8 8 8 8 8 8 7 7 7 7 7 7 8 8 8 8 7 8 7	SULT 1 18612 Alternate names: delta-aminolevu Species: Clostridium josui Jate: 16-Aug-1996 #sequence_revi Accession: 140812 Pulino, E.; Fulino, T.; Karita, Pulino, E.; Fulino, T.; Karita, Putino, E.; Fulino, T.; Karita, Pacteriol. 177, 5169-5175, 1995 Hitle: Cloning and sequencing of Reference number: A57344; MUID:9 Ceference number: A57344; MUID:9 Accession: 140812 Status: preliminary; translated Aolecule type: DNA Residues: 1-205 ARS: Tross references: GB:D28503; NID Senetics: Siperiamily: porphobilinogen syn: Asywords: carbon-oxygen lyase; h
44444444444600	thac lium #sq. #sq. #sq. #sq. #sq. #sq. #sq. #sq.
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 140812 POTPhobilinogen synthase (EC 4.2.1.24) - Clo No.Alternate names: delta-aminolevulinic acid C.Species: Clostridium josui C.Saccession: 140812 R.Fujino, E.; Fujino, T.; Karita, S.; Sakka, J. Bacteriol. 177, 5169-5175, 1995 A; Hitle: Cloning and sequencing of some gene. A; Reference number: A57344; MUID:95394829; PR A; Molecule type: DNA A; Residues: 1-205 < RES> A; Cross-references: GB:D28503; NID:9536874; CG-Genetics: A; Genetics: C; Genetics: C; Superfamily: porphobilinogen synthase C; Superfamily: porphobilinogen synthase C; Superfamily: Carbon-oxygen lyase; hydro-lyase

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α _E

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Cispecies: Vibrio cholerae
Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Rieldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833; PMID: 10952301
                                                                                                                                                                                                                                                                                                                                                                      ....... reterences: GB:AE001227; GB:AE000520; NID:g3322797; PIDN:AAC65507.1; PID:g33:
A;Experimental source: strain Nichols
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004364; GB:AE003853; NID:99657630; PIDN:AAF96157.1; GSPDB:Gh
A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable D-2-hydroxyacid dehydrogenase Cj0373 [imported] - Campylobacter jejuni (stre C; Species: Campylobacter jejuni (stre C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Gene: TP0519
C; Superfamily: response regulator of the NtrC type; response regulator homology; RNA
C; Superfamily: nesponse regulator of the NtrC type; response regulator homology <RRH>
F; 5-114/Domain: response regulator homology <RRH>
F; 143-365/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
F; 53/Binding site: phosphate (Asp) (covalent) #status predicted
F; 74/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: C81380

K; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil C.W.; Vouil, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000
                                                                                                                                                                                                                   A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                            C; Accession: F71315
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, Soon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SgaT protein VCA0246 [imported] - Vibrio cholerae (strain N16961 serogroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
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Pred. No. 30;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 23;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%; Score 49; 37.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||: | | | | ||: |:: |:: | VETAEDGNIGVEIALKGDIDLIIT 52
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                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-458 <COL>
A; Cross-references: GB:AE001227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%;
25.0%;
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Tes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                               A; Accession: F71315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: D82484
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                                                                                                                                                                                                                            Un-dependent hydrolases, glyoxylase family [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: I4-Sep-2001 #sequence_revision 14-Sep-2001 #sequence_revision 14-Sep-2001 R; Nolling, J.; Breton, G.; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4833-4838, 2001 A; Smith, D.R.
A; Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Acecession: G97070
A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein F17L21.2 [imported] - Arabidopsis thaliana Cross)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86398
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D86398
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005172; NID:99802520; PIDN:AAF99722.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 2; Length 243;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
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6; Mismatches
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                                                               Score 49;
Pred. No. 1
                            YVFSTEMANKAAEAVLKGOVETIVSFH
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WSFRSTNKAADRLAKGELENNVTF 204
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25.0%;
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Best Local Similarity 25.05
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-243 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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prolidase (Xaa-Pro dipeptidase) (pepQ) [imported] - Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 C; Accession: F90179 R: She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; C Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redde arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s. A; Racession: Ab0602; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable bacteriophage protein STY1061 [imported] - Salmonella enterica subsp. enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: GB:AE006641; NID:g13813507; PIDN:AAK40693.1; GSPDB:GN00155
C;Genetics:
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A;Cross-references: GB:AL513382; PIDN:CAD05454.1; PID:g16502215; GSPDB:GN00176
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90179
             1;
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             Mismatches
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                                                                                                             267
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                                                                                           243 SIELSQKLAAAEALIANQAEKITSF
                                                          5 STEMANK -- AAEAVLKGQVETIVSF
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             4;
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C;Superfamily: X-Pro aminopeptidase
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             Conservative
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Matches 10; Conserv
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Matches 9; Conserv
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          12;
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             Matches
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184074
Gladroxyacetone kinase BH3397 (imported] - Bacillus halodurans (strain C-125)
G.Species: Bacillus halodurans
G.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
G.Accession: B84074
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-330 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07116.1; GSPDB:GNOG
C;Genetics:
A; Fitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A; Reference number: A81250; MUD:20150912; PMID:10688204
A; Accession: C81380
A; Accession: C81380
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-311 cPAR>
A; Residues: 1-311 cPAR>
A; Cross-references: GB:AL139075; GB:AL111168; NID:96967817; PIDN:CAB74209.1; PID:9696784
A; Experimental source: serotype 02, strain NCTC 11168
A; Experimental source serotype 02, strain SCTC 11168
C; Genetics:
A; Genetics:
A; Choene: Cj0373
C; Superfamily: phosphoglycerate dehydrogenase
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Dypothetical protein T27D20.16 - Arabidopsis thaliana

Dypothetical protein T27D20.16 - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Species: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 10-Dec-1999

C.Accession: T01822

A.Species of A. thaliana T27D20.

A.Specience number: Z14441

A.Accession: T01822

A.Status: translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Rosious: 1-319 < EDM>
A.Rosious of A. thaliana T27D20.

A.Rosious: 1-319 < EDM>
A.Rosious of A. thaliana T27D20.

A.Rosious of A. thaliana tarabidopsis hypothetical protein F7N22.18

C.Superfamily: Arabidopsis hypothetical protein F7N22.18
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                                                                                                                                                                                                                                                                                                                    Length 311;
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                                                                                                                                                                                                                                                                                                              Score 48.5; DB
Pred. No. 18;
6; Mismatches
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4; Mismatches
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Pred. No.
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42.3%;
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                                                                                                                                                                                                                                                                                                              ch 35.7%;
1 Similarity 42.4%;
14; Conservative
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Best Local Similarity 42.3
Matches 11; Conservative
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Best Local Similarity
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Best Local S
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33.8%;
71.4%;
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C;Superfamily: acetate kinase
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Best Local Similarity
...thes 10; Conserve
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Best Local Similarity
Matches 10; Conserv
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change 20-Jun-2000
C;Accession: 66962
R;Kunst, F.; Oqasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997.
Nature 390, 249-256, 1997.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ;
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branched-chain fatty-acid kinase homolog yqiU - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 586;
                                                                                                                                                                                                                                                                                                                                 A)Cross-references: EMBL:U41746; PIDN:AAA83334.1; CESP:T18H9.1
C;Genetics:
A;Gene: CESP:T18H9.1
A;Introns: 23/1; 105/3; 174/3; 303/3; 403/2; 430/3; 539/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 330;
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C;Accession: T29695
R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid T18H9.
A;Reference number: Z20666
A;Accession: T29695
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-586 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 2;
Pred. No. 45;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 70;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46.5;
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A; Experimental source: strain 2035
C; Genetics:
A; Introns: 57/1; 104/1; 250/2; 293/2
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IYAFATDLARKAGQLLLE 30
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Best Local Similarity 40.7%;
Matches 11; Conservative
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Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portets Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Stakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toginoni, A.; Tosato, V.; Ochiya, Minters, P.; Wipat, A.; Tamanoto, H.; Yamane, K.; Yasumoto, R.; Tosato, V.; Uchiya, A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Rosledes: 1-461 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC48765.1; PID:g15140238; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federsplel, N.A.; Fisher, R.
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Science 293, 688-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelan hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:299116; GB:AL009126; NID:92634723; PIDN:CAB14338.1; PID:926348
A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Wolecule type: DNA
A;Residues: 1-363 <KUN>
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65;
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41.7%; Pred. No. 65;
tive 4; Mismatches
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Pred. No.
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GenCore version 5.1.6
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- protein search, using sw model protein ĕ October 15, 2003, 10:27:32; Search time 3.37743 Seconds Run on:

(without alignments)
389.867 Million cell updates/sec

US-09-915-543-15_COPY_177_204 136 1 VYVESTEMANKAAEAVLKGQVETIVSFH 28 Title: Perfect score:

Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	000512 homo sapien	drosc		P49696 fugu rubrip	-	P54532 bacillus su	-	-		Q59395 erwinia car	Q47096 erwinia car					P40614 caenorhabdi	P39301 escherichia				Q05470 bacillus su	Q17424 caenorhabdi		~		Q10269 schizosacch	Q10499 schizosacch	004462 rattus norv			7 vibrio	269	019911 cyanidium c
SUMMARLES	ID	BCL9_HUMAN	BCL9_DROME	HEM2_CLOJO	SYV_FUGRU	QUTG_EMENI	BUK_BACSU	HFA1_YEAST	SODM_CHAFE	GUNN_ERWCA	GUNW_ERWCA	GUNV_ERWCA	ZP2_MACRA	PEM3_ARATH	AIG2_ARATH	YB64_METJA	MPCP_CAEEL	SGAT_ECOLI	DNLI_AERPE	SYR_PYRFU	SYV_SCHPO	PKSL_BACSU	THI2_CAEEL	RIB4_SCHPO	EX53_MYCPN	TRPD_SULTO	AREH_SCHPO	YDGE_SCHPO	SYV_RAT	GLSL_HUMAN	NPRV_VIBPR	EMPA_VIBAN	VGLF_CDVO	SECA_CYACA
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æ	Query Match	100.0	72.1	44.1	7.	33.8	m	ω.	33.5	٠	m	m	33.5	33.1	32.7	32.4	32.4	32.4	32.4	32.4	32.4	32.4		_		31.6	31.6	31.6	•	•	٠	31.6	•	31,6
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Q15269 homo sapien P30733 solanum tub	Q921q9 mus musculu P26640 homo sapien	P93407 oryza sativ	Q8ty76 methanopyru P70955 bacillus su	05/6/2 methanococc 09vhq7 drosophila	067887 aquifex aeo 094065 candida alb
PWP2_HUMAN PHYA_SOLTU	SYV2_MOUSE SYV2_HUMAN	SODP_ORYSA	AKUD_METKA YCCH_BACSU	VATC_METUA O85B_DROME	UVRC_AQUAE MSH4_CANAL
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ALIGNMENTS

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Ii P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Berandon R.C., Rogers Y. H.C., Blazed R.G., Champe M., Prelifer B.D.,
RA Ballew R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basua A., Baxendalb G., Bardatari D., Bolshakov S.,
Bardish R.C., Baxman D.A., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Borkova D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dukov B.C., Dunn P.,
RA Gosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gul P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibegwan C.,
A Kummel B.E., Kodira C.D., Kratt C., Kennison J.A., Markellov G., Milshian N.V., Mobarry C., Morric J., Moshrefi A.,
Liu X., Mattel B., McIntosh T.C., Marchol M.P., Moshrefi A.,
RA Kummel B.E., Matthon N.V., Mobarry C., Morric J., Moshrefi A.,
RA Liu X., Mattel B., McIntosh T.C., Scheeler F., Shen H.,
Ralazolo M., Pittaman G.S., Pan S., Pollard J., Puri Y., Reses M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Ryber B., Spier E., Spradling A.C., Stapleton M., Strong R., Suit T.,
Ryber B., Reinstock G., Turner R., Venter E., Wang A.H., Wang X.,
Rybiskas R., Tector C. Turner R., Venter E., Wang X.,
Rybiskas R., Tector C., Turner R., Venter E., Wang X.,
Rybiskas R., Rodellong A., Wellenstock G.M., Weissenbach J.,
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                                                                                                                                                                                               Length 1426;
                         MIM; 602597; -.
GO; GO:0007048; P:oncogenesis; TAS.
Nuclear protein; Chromosomal translocation; Proto-oncogene;
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                               CTNNB1-BINDING.
                                                                                                                                                                                                                                                                                                                                                PRT; 1469 AA.
                                                                                                                                                                                                                       0; Mismatches
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POLY-PRO 2.
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                                                                                                                                                     POLY-PRO 3
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EMBL; Y13620; CAA73942.1; ALT_FRAME.
Genew; HGNC:1008; BCL9.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                             BCI-9 homolog (Legless protein).
BCL9 OR LGS OR CG2041.
                                                                                                                                                                           Query Match
Best Local Similarity
Local 28; Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                  Wnt signaling pathway.
DOMAIN 231 1378
DOMAIN 347 377
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331 33
514 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G->E: IN ALLELE LGS-21L.
L->F: IN ALLELE LGS-17E; SEGMENT POLARITY
                                                                                                                                                                                   STRAIN-Berkeley; TISSUE-Embryo;
MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kramps T., Peter O., Brunder E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.; "Mut, Migless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex."; cell 109:47-60(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Involved in signal transduction through the wnt pathway.
-!- SUBUNIT: Binds to ARM and PYGO.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DEVELORMENTAL STAGE: Expressed both maternally and zygotically
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 6-1469 FROM N.A., AND MUTAGENESIS OF GLY-514; LEU-534 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
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Pred. No. 1.6e-06;
9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :->K: IN ALLELE LGS-17P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 IFVFSTQLANKGAESVLSGQFQTIIAYH 350
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GLN-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21952490; PubMed=11955446;
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1469 AA;
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Les 16; Conserv
                                                                                                                                                                    SEQUENCE FROM N.A.
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1340
1162
514
534
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Q59295;
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DOMAIN
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HEM2_CLOJO
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Matches
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QUTC_EMENI
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) (Porphobilinogen
                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARAIN-FERR P-0698
MEDLINE-953948299, PubMed-7665501;
Fujino E., Fujino T., Karita S., Sakka K., Ohmiya K.;
Fujino E., Raino T., Karita S., Sakka K., Ohmiya K.;
Fujino E., Raino T., Karita S., Sakka K., Ohmiya K.;
Diosynthesis from the anaerobic bacterium Clostridium josui.";
J. Bacteriol. 1777:5169-5177(1995).
-1- CATALYTIC ACTIVITY: 2 5-aminolevulinate = porphobilinogen + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valy1-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS)
                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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Pred. No. 0.1;
5; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23172 MW; 886F9DAEFDB1144E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00144; DALDHYDRTASE.
ProDom; PD002304; Alab_dehydratase; 1.
PROSITE; PS00169; D_ALA_DEHYDRATASE; PARTIAL.
                                                                                                                                                                                                                                                                                  -1- COFACTOR: Zinc (By similarity).
-1- PATHWAY: Siroheme biosynthesis.
-1- SUBUNIT: Homooctamer (By similarity).
-1- SIMILARITY: BELONGS TO THE ALADH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1217 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001731; Alab_dehydratase.
Pfam; PF00490; ALAD; 1.
                                                          synthase) (ALAD) (ALADH) (Fragment).
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MEDLINE=97396021; PubMed=9254008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphyrin biosynthesis; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D28503; BAA05863.1; -.
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                                                                                    Clostridium josui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31033;
                                                                                                                  Clostridium.
NCBI_TaxID=1499;
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P49696;
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SEQUENCE
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Lim E.H., Corrochano L.M., Elgar G., Brenner S.; "Genomic structure and sequence analysis of the valy1-tRNA synthetase gene of the Japanese pufferfish, Fugu rubripes.";
DNA Seq. 7:141-151(1997).
-!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate + L-valy1-tRNA(Val).
-!- SIMILARITY: Belongs to class-1 aminoacy1-tRNA synthetase family.
-!- SIMILARITY: THE N-TERMINAL DOMAIN IS SIMILAR TO ELONGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding. DOMAIN 1 2320
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Lamb H.K., Hawkins A.R., Smith M., Harvey I.J., Brown J., Turner G.,
Roberts C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Spatial and biological characterisation of the complete quinic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89181521; PubMed-2976880; Hawkins A.R., Lamb H.K., Smith M., Keyte J.W., Roberts C.F.; Hawkins A.R., Lamb H.K., Smith M., Keyte J.W., Roberts C.F.; Molecular organisation of the quinic acid utilization (QUT) gene cluster in Aspergillus nidulans."; Mol. Gen. Genet. 214:224-231(1988).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1217;
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"KMSKS" REGION.
ATP (BY SIMILARITY).
WW: 5E08AF24B5C8A7A1 CRC64;
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Mol. Gen. Genet. 223:17-23(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%; Score 51; 37.0%; Pred. No. :
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SIMILARITY TO INOSITOL MONOPHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00986; TRNAŠYNTHVAL.
TIGRFAMS; TIGR00422; valS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004046; GST_Cterm.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002333; tRNA-synt_val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138218 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00043; GST_C; 1.
Pfam; PF00133; tRNA-synt_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X91856; CAA62967.1; -. HSSP; P96142; 1GAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.5
Best Local Similarity 37.0
Matches 10; Conservative
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                                                                                                                                                                                                     FACTOR 1-GAMMA.
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SEQUENCE FROM N.A.
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Matches
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A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
B Borriss R., Boursier L., Brans A., Broun M., Brignell S.C., Bron S.,
B Brouillet S., Bruschi C.V., Caddwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Gims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Kurita K., Lapidus A., Latdinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many sporulation genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato I., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable butyrate kinase (EC 2.7.2.7) (BK) (Branched-chain carboxylic acid kinase).
FUNCTION: NOT KNOWN. PROBABLY INVOLVED IN QUINATE METABOLISM. SIMILARITY: Belongs to the inositol monophosphatase family.
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                33.8%; Score 46; DB 1; Length 330; 38.9%; Pred. No. 21; ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                     330 AA; 36762 MW; 11CD80C65E077A24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                    PIR; S08500; S08500.
HSSP; P29218; 1IMF.
InterPro; IPR00760; Inositol_P.
Probom; PD023420; Inositol_P; 1.
PROSITE; PS00629; IMP_1; 1.
PROSITE; PS00630; IMP_2; 1.
                                                                                                                                                        EMBL; X13525; CAA31878.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                          :| |:|::| || : :|:
13 IYAFATDLARKAGQLLLE 30
                                                                                                                                                                                                                                                                                                                                                                          1 VYVFSTEMANKAAEAVLK 18
                                                                                                                                                                                                                                                                                                                                Local Similarity 38.9 ses 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                        Quinate metabolism.
SEQUENCE 330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUK_BACSU
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
BUK_BACSU
                                                                                                                                                                                                                                                                                                                                              Matches
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A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Rieger M., Rivolta C., Rocha B., Rapport G., Rey M., Reynolds S.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Sckowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchlyama S., Vandenbol M., Vannier F., Vasarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasarotti A.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
T. "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
--- CATALIYIC ACTIVITY: ATP + 2-butanoate = ADP + butanoyl phosphate.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the acetokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFA1 protein.
HFA1 OR YMR207C OR YM8261.01C OR YM8325.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 2273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Kinase; Complete proteome
SEQUENCE 363 AA; 39764 MW; 94ADA51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01075; ACETATE_KINASE_1; 1. PROSITE; PS01076; ACETATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF_00542; -; 1.
InterPro; IPR000890; Acetate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00871; Acetate_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00471; ACETATEKNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D84432; BAA12596.1; -. EMBL; 299116; CAB14338.1; -. PIR; C69962; C69962. SubtiList; BG11724; buk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AAEAVLKGQVETIV 25
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STRAIN=S288c / AB972;
PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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P32874;
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PRANSIT
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Matches
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                   SIMILARITY: STRONG, TO ACETYL-COA CARBOXYLASE.
CAUTION: THE READING FRAME FROM WHICH THIS PROTEIN IN TRANSLATED
HAS NO MET INITIATION CODON NEAR TO THE 5'END. IT DOES NOT SEEM TO
BE A PSEUDOGENE. THERE ARE NO APPARENT FRAMESHIFTS.
                                                   Kearsey S.E.; Identification of a Saccharomyces cerevisiae gene closely related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
L6-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Superoxide dismutase (Rml, mitochondrial precursor (EC 1.15.1.1).
Charybdis feriatus (Crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.8%; Score 46; DB 1; Length 2273; Best Local Similarity 45.0%; Pred. No. 1.5e+02; Matches 9; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Charybdis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY).
BY SIMILARITY.
BIOTIN (BY SIMILARITY).
F -> L (IN REF. 2).
WW; 08727A301549DA92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AA.
                                                                                                                                                                                                                                                                                              EMBL, 249809; CAA89922.1; --
EMBL, 248755; CAA8847.1; --
EMBL, 222558; CAA80280.1; --
PIR, 555089; S55089.
HSSP: P24182; IDV1.
SGD; S0004820; HFA1.
InterPro; IPR001882; Biotin_attach.
InterPro; IPR001882; Biotin_lipoyl.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR005482; Biotin_lipoyl.
InterPro; IPR005482; Biotin_lipoyl.
Pfam; PF02785; Biotin_carb_C.
Pfam; PF02785; Biotin_carb_C.
Pfam; PF02785; Biotin_lipoyl; I.
Pfam; PF00284; CPSase_L.C.
Pfam; PF00286; CPSase_L.C.
PF0021E; PS001188; BIOTIN; I.
                                                                              FAS3 (acetyl-CoA carboxylase).";
DNA Seq. 4:69-70(1993).
-1- COFACTOR: BIOTIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 125-949 FROM N.A. MEDLINE=94146412; Pubmed=7906156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YVFSTEMANKAAEAVLKGQV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259160 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO086; CPSASE_1; 1.
PROSITE; PS0086; CPSASE_1; 1.
Biotin; Ligase; Arp-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661
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2273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=65693;
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096347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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Lin C.T., Lai Y.S., Kuo T.J., Chang T.C.;
"Molecular cloning, expression, and characterization of a cDNA
encoding Mn-superoxided dismutase from crab Charybdis feriatus.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Atroseptica FCBR C18;
MEDLINE-9829944; PubMed-9636315;
Olsen O., Thomsen K.K., Weber J., Duus J.O., Svendsen I., Wegener C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: Homotetramer (By similarity).
-1- SUBCELLULAR LOCATION: Mitochondrial matrix.
-1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase N precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDEION (BY SIMÎLÂRITY).
SODEROXIDE DISMUTASE [MN].
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Manganese; Mitochondrion; Transit peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 AA.
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 YVNNLNVAEEKLAEAKEKGDVSTIIS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YVFSTEMA-NKAAEAVLKGQVETIVS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPP/01189; SODismutase. Pfam; PF00081; sodfe; 1. Pfam; PF01777; sodfe_C; 1. Probom; PD000475; SODismutase; 1. PROSITE; PS00088; SOD_MN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 MA
94 MA
177 MA
181 MA
24527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF019411; AAD01640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Cellulase N)
                                                                                                                                                                                                                                        FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUNN_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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us-09-915-543-15_copy_177_204.rsp

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CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
GUNV_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                          Matches
        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE=57231512; PubMed=7715600;
Mae A., Heikinheimo R., Palva E.T.;
"Structure and regulation of the Erwinia carotovora subspecies
carotovora SCC3193 cellulase gene celV1 and the role of cellulase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase VI precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase VI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linkages in cellulose, lichenin and cereal beta-D-glucans.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phytopathogenicity.;
Mol. Gen. Genet. 247:17-26(1995).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                      444 ENDOGLUCANASE N.
168 PROTON DOMOR (BY SIMILARITY).
256 NUCLEOPHILE (BY SIMILARITY).
48300 WW. FA7E4179004CBB43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                      EMBL; LJ5700, LD5700, LD5700, LD5700, LD585, LD57001956; LD57001956; LD57001956; LD57001956; LD57001956; LD57001950; LD5700195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YVFSTEMANKAAEAVLKGQ----VETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45.5;
Pred. No. 33
                                                                                                                                                                                                    EMBL; L39788; AAC37033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.5%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X79241; CAA55823.1; -. PIR; S54744; S54744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      444
168
256
                                                                                                                                                                                                                                                                                                                                                                                                                                          256
444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Cellulase V1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SCC3193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUNW_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUNW_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooper V.J.C., Salmond G.P.C.; "Molecular analysis of the major cellulase (CelV) of Erwinia carotovora: evidence for an evolutionary 'mix-and-match' of enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
NCBL_TaxID=554;
                                                                                                                                                                                                                        CATALYTIC.
LINKER.
CELLULOSE-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 504;
                                                                                                                                                                                                                                                                                      PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
0D7ECF74781565FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
HSSP; O85465; 1A3H.
Interpro; IPR001956; CBD_3.
Interpro; IPR001547; Glyco_hydro_5.
Pfam; PF00942; CBM_3; 1.
Pfam; PF00150; cellulase; 1.
Procom; PF001947; CBD_3; 1.
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                       ENDOGLUCANASE V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505 AA
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 38;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YVFSTEMANKAAEAVLKGQ---VETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                   Score 45.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, 085465; 1A3H.
InterPro; IPR001956; CBD_3.
InterPro; IPR001547; Glyco_hydro_5.
Pfam; PF00942; CBM_3; 1.
Pfam; PF00150; cellulase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94067016; PubMed=8246888;
                                                                                                                                                                                                                                                                                                                                       54963 MW;
                                                                                                                                                                                                                                                                                                                                                                            33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X76000; CAA53592.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S39962; S39962.
                                                                                                                                                                                                32
32
32
32
353
353
168
168
256
264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SCRI193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Cellulase V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUNV_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domains.";
                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                     Ξ;
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Reprod. Dev. 50:229-239(1998).
-1-FUNCTION: ZPZ FORMS WITH ZP1 AND ZP3 THE ZONA PELLUCIDA, IN
FUNCTION: ZPZ PORMS WITH INTO COPOLYMERS CROSS-LINKED BY ZP1.
ZP2 ACTS AS A SECONDARY SPERM RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: IS PROTEOLYTICALLY CLEAVED AFTER FERTILIZATION, AND THIS MODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 MAY PLAY AN IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO POLYSPERMY. PTM: SULFATED GLYCOPROTEIN WITH 0-LINKED OLIGOSACCHARIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                               15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-2000 (Rel. 39, Last annotation update)
200-MAY-2000 (Rel. 39, Last annotation update)
20na pellucida sperm-binding protein 2 precursor (Zona pellucida
glycoprotein ZP2) (Zona pellucida protein A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein. Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00662; ZP_DOMAIN; 1.
Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;
Extracellular matrix.
                                                                                                                 CELLULOSE-BINDING (BY SIMILARITY).
PROTON DONG (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
DBRA9337BA4D2623 CRC64;
                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Ovary;
MEDLINE-99250422; PubMed-9590540;
Jethanandani P., Santhanam R., Gupta S.K.;
Molecular cloning and expression in Escherichia coli of cDNA
                                                                                                                                                                                                  Length 505;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding bonnet monkey (Macaca radiata) zona pellucida glycoprotein-2P2.";
ProDom; PD001947; CBD_3; 1.
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal.
                                                                                                                                                                                                    DB 1;
                                                                 ENDOGLUCANASE V.
                                                                                                                                                                                                                                                                                        101 YISNPSLANKVKEAVAAAQSLGVYIIIDWH 130
                                                                                                                                                                                                                                                                                                                                                                                     745 AA
                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                   Pred. No. 38;
                                                                                                                                                                                                                                                                    2 YVFSTEMANKAAEAVLKGQ---VETIVSFH 28
                                                                                                                                                                                                    Score 45.5;
                                                   POTENTIAL.
                                                                                CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 ZP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
                                                                                                   LINKER
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca radiata (Bonnet monkey).
                                                                                                                                                                   54900 MW;
                                                                                                                                                                                                 33.58;
36.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y10690; CAA71693.1; -.
                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae: Macaca
                                                                 505
334
352
505
505
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                32
335
353
168
256
505 AA;
                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matrix.
                                                                                                                                                                                                                                                                                                                                                                                    2P2_MACRA
077726;
                                                                                                                 DOMAIN
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                  DOMAIN
DOMAIN
                                                   SIGNAL
                                                                   CHAIN
                                                                                                                                                                                                                                     Matches
   ŏ
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Theologis A., Ecker J.R., Palme C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palme C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Burhler E., Chan A., Chao Q., Chan H., Cheuk R.F., Chin C.W.,

A. Chung M.K., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

R. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,

R. All J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. A. Lin S.Y., Liu Z.A., Luros J.B., Kwan A., Lia B.,

R. Langin-Hooper S., Lee A., Lucos J.S., Malti R., Mazziali A.,

R. Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

R. Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Tortumi M.J., Town C.D.,

R. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Catalyzes N-methylation of phosphoethanolamine, phosphomonomethylethanolamine and phosphodimethylethanolamine, the three methylation steps required to convert phosphoethanolamine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 4), Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, La
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                            PELLUCIDA SPERM-BINDING PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphocholine (By similarity).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + ethanolamine
phosphate - S-adenosyl-L-homocysteine + N-methylethanolamine
                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                            (GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                          .
6
                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    731D9AFA4D3EE028 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                     ZP.

N-LINKED (GLCNAC...) (
                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : | : | | : | | 382 VYSYQTQPALDLDTLRVGNSSCQPVFKAQSQGLVRFH 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VYVFSTEMA-----NKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 AA
                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 57;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 45.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished observations (MAY-2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
                            ZONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                    82710 MW;
                                                                                                                                                                                                                                                                                                                                                                    33.5%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONCEPTUAL TRANSLATION.
38
745
745
745
637
637
1122
223
310
400
                                                                                                                                                                                                                                                                                                                    745 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
  1
39
39
717
717
737
370
87
105
122
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schneider M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEM3_ARATH
Q9C6B9; Q90
                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana.
                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                               CARBOHYD
                      CHAIN
                                                                                                DOMAIN
                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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YB64_METJA
ID YB64_METJA
AC Q58564;
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                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                              HIDDEN NEW WENT AND DESCRIPTION OF STREET AN
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reuber T.L., Ausubel F.M.; "Isolated differentiate between resistance "Isolation of Arabidopsis genes that differentiate between resistance responses mediated by the RPS2 and RPM1 disease resistance genes."; Plant Cell 8:241-249(1996)
                      CAUTION: Ref.1 (AAG51806) sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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  SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              SAM-BINDING 1.
SAM-BINDING 2.
77FDFAFBC89C41CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U40857; AAC49283.1; -.
EMBL; AB025615; BAA95744.1; -.
SEQUENCE 170 AA; 19445 MW; A4C4F6417143AE30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 44;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIG2 OR AT3G28930 OR K5K13.3 OR K5K13_1.
                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Methyltransferase; Repeat.
                                                                                                                                                                                                                                                                                         EMBL; AC079676; AAG51806.1; ALT_SEQ.
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STRAIN-cv. Columbia;
MEDLINE-20277480; PubMed-10819329;
                                                                                                                                                                                                                                                                                                                EMBL; AC012679; AAG52075.1; -.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSTEMANKAAEAVLKGQVETIV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTTELAQKAGQVIAVDFIESVI 87
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STRAIN-cv. Columbia;
MEDLINE-96351417; PubMed-8742710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56368 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Bost Local Similarity 31.00.
Bost Local Similarity 7. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:131-135(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                                                                                                                     278
490 AA;
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P54121:
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STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Eleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlawage A.R., Doughherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.

Utterback T.K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE PBSX(XRE) FAMILY OF TRANSCRIPTIONAL REGULATORS. ARCHAEAL 1 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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      DB 1; Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 318;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical transcriptional regulatory protein MJ1164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococus.
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318 AA; 36529 MW; F7E61B67F09263CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9
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                                                                                                                                                                                                                                                                                                                                                          318 AA
                                 Pred. No. 18;
0; Mismatches
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      Score 44.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: October 15, 2003, 10:31:00
                                                                                                                                                                                              TEYVRKTVEVVLIDILEKKOVETIV 109
                                                                                                                              6 TEMANKAAEAVL----KGQVETIV 25
                                                                                                                                                                                                                                                                                                                                                          PRT;
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156 IYKYETQMANPSVDVALK 173
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Query Match 32.7%;
Best Local Similarity 52.0%;
Matches 13; Conservative
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InterPro; IPR001387; HTH_3.
Pfam; PF01381; HTH_3; 1.
SWART; SM00530; HTH_XRE; 1.
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Best Local Similarity
7; Conserve
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DNA_BIND 142
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097769 candida gla 081x99 homo sapien 08xx5 clostridium 08x163 bartonella 081460 arabidopsis 098069 sulfolobus 08pln0 streptococc 08rv4 lycopersico 08zy3 mus musculu 08z13 salmonella 08z13 salmonella

096250 097687 091735 091735 081179 081789 081460 098069 088140 098079 08714 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09220 08814 09270 08814 09220 08814 09220 08814 09270 08814 09270 08814 09270 08814 09220 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09270 08814 09220 08814 09270 08814 08

Q8wzx5 neurospora Q8mmt3 dictyosteli Q8myg5 dictyosteli O71209 grapevine l Q8efd3 shewanella

022551 caenorhabdi 019380 caenorhabdi 08ijx6 plasmodium

ALIGNMENTS

096497 trypanosoma 096250 sulfolobus 0976p7 sulfolobus 097794 bacillus ha 091v35 arabidopsis 08bin9 mus musculu

Q9pic9 campylobact O96497 trypanosoma

Q8tfzl asperqillus

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Run on:

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476
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SEQUENCE FROM N.A.
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01-MAY-2000
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 290104
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08521 capsicum ch
096612 homo sapien
096912 homo sapien
096919 lactobacill
09147 arabidopsis
09769 sulfolobus
089383 bifidobacte
09f211 arabidopsis
09629 sulfolobus
096x55 sulfolobus
096x55 sulfolobus
096x55 vibrio vuln
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09v611 drosophila
0960e6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9u1q4 caenorhabdi
                                                                                                                                          (without alignments)
445.097 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                          October 15, 2003, 10:27:33 ; Search time 16.2335 Seconds
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                                                                                                                                                                                                                                                                                                                                                           830525
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
                                                                                                                                                                                              US-09-915-543-15_COPY_177_204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9U1Q4
Q97JA0
Q9V6L1
Q960E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_mammal:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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seq length: 200000000
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sp_bacteria:*
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sp_human:*
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Match
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Maximum DB
                                                                                        OM protein
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                                                                                                                                                                                   Y87G2A.5 protein.
Y87G2A.5.
Caenorhabditis elegans.
Caenorhabditidae; Rhabditidae; Rhabditoidea;
Rhabditidae, Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRRAMS; TIGRO0422; vals; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
SEQUENCE 1050 AA; 118920 WW; F33DB55587EAC057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55; DB 5;
Pred. No. 22;
PRT; 1050 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL, Ali10500, CAB60428.1; -.
EMSP, P96142: 1GAX.
Wormbep; Y87G2A.5; CE24685.
InterPro; IPR001300; tRNA-synt_1.
InterPro; IPR001310; tRNA-synt_1.
Pfam; PF00133; tRNA-synt_1: 1.
PRINTS; PR001865; TRNA-SYNT_1.
                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.48;
                                                                       01-MAY-2000 (TYEMBLRel. 13, 01-MAY-2000 (TYEMBLRel. 13, 01-MAR-2003 (TYEMBLRel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
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Best Local Similarity
Matches 12; Conserv
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082521 0946R2 096GN2 096Q02 08GG19 091FW7 0976C9

642 642 1098 350

Result No. Q9FZL1 Q96YA9 Q96X55 Q8DFX2

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STRAIN—ATCC 824 / DSM 792 / VKM B-1787;
STRAIN—E4155935; Dubmed=11466586;
Nebling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2019606; PubMed=10731132; Adams M. Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ball W. M., Baxendalle J., Bayraktarcollu L., Beasley E.M., Beeson K.Y., Bernan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.5%; Score 51; DB 16; Length 243; 25.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
Hydrolase; Complete protecome.
SEQUENCE 243 AA; 26880 WW; 0F9F6A3EAADEBCOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
2n-dependent hydrolases, glyoxylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1049 AA.
                                                                                                                                                                                 243 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: | : :: | : | : | : | : | 199 LFDFDSNLSKKSLEKLTKYDIETVICYH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VYVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                             461 YVKCAHMAEKAVAAVANGDLQIIPEFH 487
                2 YVFSTEMANKAAEAVLKGQVETIVSFH
                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE007650; AAK79354.1; -.
                                                                                                                                                                                                                           (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG4062 protein.
AATS-VAL OR CG4062.
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                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1488;
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                                                                                                                                                                                                                         01-OCT-2001
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Q9V6L1
                                                                                                                                 RESULT 2
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Wu C., Lewis S.E., Rubin G.M., Celniker S.;

Nunco J., Pardeb J., Paragas V., Park S., Phouanenavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases.

BR Hybase: FB900027079; Aats.val.

DR FILEPTO: IPR001303; LRNA-synt_la.

DR InterPro: IPR001303; LRNA-synt_la.

DR Fidn; PF00133; LRNA-synt_la.

DR Pfan; PF00133; LRNA-synt_la.

DR Pfan; PF00133; LRNA-synt_la.

DR Pfan; PF00134; LRNA-synt_la.

DR Pfan; PF00134; LRNA-synt_la.

DR Pfan; PF00134; LRNA-synt_la.

TIGRFAMS; TIGR00422; valS; l.

DR PROSITE; PS00178; AA_TRNA_LIGASE_I; l.
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative aminotransferase.
Capsicum chinense.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermātophyta; Magnoliophyta; ēudicōtyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Capsicum.
NCBL_TaxID=80379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 51; DB 5; Length 1049; 40.7%; Pred. No. 89;
                                  37.5%; Score 51; DB 5; Length 1049; 40.7%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                             11; Indels
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1. SEQUENCE 1049 AA; 118253 MW; 13A513ABF69E8EEB CRC64;
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. AF085149) from Habanero Chile. (PGR98-182).";
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                                                                                                                                                                              PRT; 1049 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 YVSCSDMAASATEAVRSGELKIIPEHH 497
                                                                                                     2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 40.7
Matches 11; Conservative
                                                             11; Conservative
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                                                                                                                                                                                                                                            SD04748p.
AATS-VAL OR CG4062.
                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-7227;
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                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        082521;
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                                                               Matches
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Q960E6
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                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                  DB 10; Length 459;
51;
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Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK025618; BAB15191.1;
HSSP; P96142; IGAX.
Plant Physiol. 118:1102-1102(1998).
EMBL; AF085149; AAC78480.1; -.
HSSP; P04181; 20AT.
InterPro; IPR005814; Aminotrans_3.
Pfam; PF00202; aminotran_3; 1.
PROSITE; PS00600; AA_TRNGFER_CLASS_3; 1.
Aminotransferase; Transferase
SEQUENCE 459 AA; 50729 MW; 02ABB4D728B524E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 642 AA; 71578 MW; C9E37EE1D742B7F1 CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
01-OCT-2002 (TrEMBLrel, 22, Last annotation update)
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41.7%; Pred. No. ol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                              196 FSTRLANNLESLILKEGPETVAAF 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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InterPro; IPR002303; tRNA-synt_val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein FLJ21965.
Homo sapiens (Human).
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Atches 10; Conservative
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es 12; Conservative
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FROM N.A.

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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                               Score 50; DB 4; Length 642; Pred. No. 73; 4; Mismatches 11; Indels
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Lactobacillus.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR002303; tRNA-synt_val.
Pfam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00986; TRNASYNTHVAL.
Hypothetical protein.
SEQUENCE 642 AA; 71650 MW; IF00CBB73742B579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA1885 (Fragment).
KIAA1885.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                       2 YVFSTEMANKAAEAVLKGQVETIVSFH 28
                                                                                                                                                                                                                                                                                                                                                                                                FVRCQEMGARAAKAVESGALELSPSFH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00986; TRNASNTHVAL.
TIGRPAMS; TIGR00422; vals; 1.
PR0SITE; PS00178; AA_TRNA_LIGASE_1; 1.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               large proteins.";
DNA Res. 8:179-187(2001).
EMBL. AB067472; BAB67778.1; -.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002303; tRNA-synt_l.
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MEDLINE-21456161; PubMed-11572484;
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(TrEMBLrel. 23, I
(TrEMBLrel. 23, I
                                                                                                                                                                                                   Query Match
Best Local Similarity 44.4%;
Matches 12; Conservative
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Best Local Similarity
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01-MAR-2003 (
01-MAR-2003 (
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee Z., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
                       Bringel F., Hubert J.-C.;
"Investigation of arginine requirement in Lactobacillus isolated from different environments revealed point mutations, insertions and deletions in arginine biosynthetic genes.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF514870; AAO15990.1; -. 64D1986ED73C8AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou T., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence for Arabidopsis thallana BAC 77N9 from chromosome
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ک
                                                                                                                                                                                                                                                                                                                                  DB 2; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                               36.4%; Score 49.5; Dilarity 54.5%; Pred. No. 45; Conservative 4; Mismatches
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176 VYSTDLLAKAAE---KGQVDAI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VFSTEMANKAAEAVLKGQVETI 24
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 12; Conserv
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STRAIN-CCM3626;
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01-MAR-2001
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                                                                                                                                                                                                                Q9FZL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                          Gaps
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC000348; AAF79866.1; - 6FEC48B07326B313 CRC64;
                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-NCC 2705;
MEDLINE-2224977; PubMed-12381787;
Scholl M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 143;
                                                                   Length 141;
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                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D1AFCC5157298CA2 CRC64;
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                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein ST0252.
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                                                                  DB 10;
19;
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                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 VLVVLTNMKNVEKEAEKVLKTRIDKVVYIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome SEQUENCE 143 AA; 16822 MW; DIAFCC519
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                                                                  Score 49;
Pred. No.
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                                                                                                                               112 WSFRSTNKAADRLAKGELENNVTF 135
                                                                                                               4 FSTEMANKAAEAVLKGQVETIVSF 27
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EMBL; AP000982; BAB65218:1; -.
                                                                   36.0%;
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Matches 13; Conservative
                                                                               Local Similarity 41.7 nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                          STRAIN=JCM 10545 / 7;
PubMed=11572479;
                                                                                                                                                                                                                                                                        Sulfolobus tokodaii
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NCBI_TaxID=111955;
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Pridmore R.D., Arigoni F.;
"The genome sequence of Bifidobacterium longum reflects its adaptation
to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL: AE014802. AAN25468.1;
Glycosyltransferase; Transferase; Complete proteome.
SEQUENCE 187 AA. 20617 MW; E697C3C127277DBI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Chol E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Law B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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26;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ACCO4657; AAF99722-1; -
INTERPRO; IPRO03822; PAH.
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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45.2%; Pred
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Submitted (DEC-1998)
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Submitted (AUG-2000)
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PubMed=11572479;
Kawarabayasi Y. Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ST1165.
ST1165 OR ST0857.
Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
NGBL_TAXID-111955;
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Ouery Match 36.0%; Score 49; DB 10; Length 210; Best Local Similarity 41.7%; Pred. No. 30; Matches 10; Conservative 6; Mismatches 8; Indels
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DNA Res. 8:123-140(2001).
ENBL; AP000989; BAB67368.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 233 AA; 27253 MW; 8B9E6FDB60EEE36D CRC64;
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Crenarchaeon, Sulfolobus tokodaii strain7.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein ST2259.
ST2259.
Sulfolobus tokodaii.
                                                                                                                                                                                                                                                                                                                                              233 AA.
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PubMed=11572479;
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NCBI_TaxID=111955;
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2. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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5. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
7. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
9. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
11. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
12. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
14. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
15. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
16. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
17. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
18. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
19. SIDSI/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                              October 15, 2003, 10:27:32 ; Search time 119.268 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-915-543-15_COPY_199_392
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect
                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human legless homo	Human BCL9 homolog	Human polypeptide	Mouse beta-catenin	Mouse beta-catenin	Human polypeptide	WASP homolog prote	Amino acid sequenc	Novel human diagno
ID		ABB11808	AA005855	-	AAU78460	_	_		ABG27250
DB	23	22	22		•	22	. •	22	22
Length	1426	1435	140	320	1494	707	574	574	406
% Query re Match Length DB I	100.0	100.0	26.9	22.6	22.6	16.3	15.8	15.8	15.5
Score	1028	1028	277	232.5	232.5	167.5	162.5	162.5	159
Result No.	1	7	3	4	2	9	7	8	σ

Peter 0;

Froesch B, Kramps T,

Basler K, Brunner E,

mammary	Human mammary carc	phila me	Mouse neural Mena+	Mouse neural Mena+	Mouse neural Mena+	Mammalian enabled	Novel human diagno	Human mammary carc	Mycobacterium tube	Mycobacterium tube	Protein encoded by	Herbicidally activ	Human mammary carc	Human extensin hom	Human polypeptide	Human H-2RIIBP. H	Retinoid C recepto		х P	etinoid X	ָס	×		×	Human retinoid X r	Human retinoid X r	Human retinoid X r	Н	Human retinoid X r		Human retinoid X r	Human retinoid X r	retinoid	×	Human retinoid X r	
ABU52945	ABU52939	ABB70063	AAW37151	AAW37152	AAW37153	σn.	ABG14000	ABU52937	AAW31855	AAW31852	AAB74209	ABB93202	ABU52946		ABP69529	AAR72483	ABB79960	AA019271				on										AA019296	AA019297		AA019299	
22	77	22	5	19	13	22	22	22	18	18	22	23	22	22	23	16	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	
256	•		77	ന	\circ	\circ	an.	S	~	S	m	3	\sim	₩.	σ	3	m	m	m	m	\sim	ന	m	ന	ന	ന	m	m	G)	m	(T)	(T)	(41	(7)	(*)	
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158.5	2	58.	n	S	S	S	S	S	വ	വ	<u>.</u> ;	•	53.	51.	S	50.	150.5	50.	50.	50.	50.	50.	50.	50.		50.	50.	50.	50.	50.	50.	50.	50.	50.	50.	
10	11	12	33	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	4.5	

ALIGNMENTS

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Legless; human; 1gs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                  Human legless homologue 1gs/bc19 protein.
                     AAB71229 standard; Protein; 1426 AA.
                                                                                                                                                                                                                          27-JUL-2001; 2001US-0915543.
                                                                                                                                                                                                                                                 28-JUL-2000; 2000US-221502P.
                                                               (first entry)
                                                                                                                                                                                                                                                                    BASLER K.
BRUNNER E.
FROESCH B.
                                                                                                                                                                                                                                                                                                     KRAMPS T.
PETER O.
                                                                                                                                                                               US2002086986-A1.
                                                                                                                                                             Homo sapiens.
                                                              18-NOV-2002
                                                                                                                                                                                                    04-JUL-2002.
                                          AAB71229;
                                                                                                                                                                                                                                                                                                     (KRAM/)
(PETE/)
                                                                                                                                                                                                                                                                     (BASL/)
                                                                                                                                                                                                                                                                                            (FROE/)
                                                                                                                                                                                                                                                                                (BRUN/)
RESULT 1
           AAB71229
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Fang YT, Liu C, Drmanac RT

(HYSE-) HYSEQ INC.

05-FEB-2001; 2001WO-US03800. 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

09-AUG-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; growth factor;
haematopoiesis regulation; tissue growth; immunomodulator; activin;
inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGSNSSSADPKAPPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK 180
                                                                                                                                                                 This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Mnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoms or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (1gs) protein homologue 1gs/bc19 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
                                                                         polypeptide useful in therapeutic method for treating disorders .1 fate such as cell differentiation or cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation; metastasis; cancer; tumour; haematopoietic disorder; metastasis; cancer; tumour; haematopoietic disorder; method cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischeemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1028; DB 23; Length 1426;
Pred. No. 7.5e-65;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human BCL9 homologue, SEQ ID NO:2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB11808 standard; peptide; 1435 AA.
                                                                                                                                    Example II; Fig 8B; 41pp; English.
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                  2002-635689/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 194; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1426 AA;
                  WPI; 2002-635689
N-PSDB; AAF88467
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                                                                                                 cell
                                                                           Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Comparation also relates to vectors and recombinant host cells encoding them. The invention also relates to vectors and recombinant host cells comprising a nuclectide of the invention, methods of producing them notel polypeptides, and recombinant host cells comprising a nuclectide of the invention, methods of producing the novel polypeptides, and nucleotide of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the complypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; stem cell growth factor activity; have various activity; activity; tissue growth activity; activity; activity; activity; tissue growth activity; activity; activity; activities; themmological activities; haemostatic, thromboly continuon activities; ander cell proliferation or metastasis.

Commondulatory activities; receptor or ligand activities; or ameliotrating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions include activities in activity may be used to promote wound become activity and borner or pepalic (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incliders and elucitions and ulcers), while those with healing (e.g., of burns, incliders and puppetides may be used to promote cell growth. For example, such polypeptides may be used to augment or replace the manipulate stem cells in addition the near conditions and ulcers) and annipulate stem cells in culture to give rise to neuroepithelia per manipulate stem cells in culture to give rise to neuroep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIPAPAPARPARPREDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
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                                                                                                                                                                                                                                                                                                                                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1028; DB 22; Length 1435; 100.0%; Pred. No. 7.6e-65; o. Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 256-257; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide of the invention.
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                                                                                                                                                                                                                                                                  2001-457740/49.
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protein; cancer;

(first entry)

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New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to a beta-catenin nuclear localised protein
                                                                                                                           Mouse beta-catenin nuclear localised protein #2.
                                                                                                                                                     Mouse; beta-catenin nuclear localised
                                                                                                                                                                     gene therapy; EST; expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 91-92; 113pp; Japanese.
                                         AAU78461 standard; Protein; 320 AA.
                                                                                                                                                                                                                                                                              19-SEP-2001; 2001WO-JP08140.
                                                                                                                                                                                                                                                                                                          22-SEP-2000; 2000JP-0287876.
                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO
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                                                                                                                                                                                                                                                                                                                                                                  Akiyama T, Adachi
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABK47632
                                                                                                                                                                                                                         WO200224738-A1
                                                                                                                                                                                                Mus musculus.
                                                                                               02-JUL-2002
                                                                                                                                                                                                                                                    28-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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               RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
 QGSNSSSADPKAPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK 180
                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patent did not form part of the printed in electronic format directly from WIPO
             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 19747; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 277; DB 22;
Pred. No. 1.7e-12;
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                     AA005855 standard; Protein; 140 AA.
                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 19747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.9%;
91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                               EFTGAQSGGPQONP 432
                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927
                                                       EFTGAQSGGPQQNP 194
                                                                                                                                                                                                            (first entry)
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Best Local Similarity 91.4:
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAI85786
                                                                                                                                                                                                                                                                                                                                                              WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification,
                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation
                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                               AA005855;
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121
                                                     181
                                                                                                                         RESULT 3
                                                                                                                                        AA005855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILAYHQQNVPRAKLDQA------PKVPPTPEPLPLN---TPSAGTPQSQPP
                                                                                                                                                                                                                                                                                                        1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLPPPPPAPGSAPPALPPEGPPEDTSQDLAPNSVG--AASTGGGTGGTHPNTPTAATANN
and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein #2.
                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                            75; Indels
                                                                                                                                                                                                          DB 23;
                                                                                                                                                                                                          22.6%; Score 232.5; DB 35.1%; Pred. No. 5.7e-09;
                                                                                                                                                                                                                                                            23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU78460 standard; Protein; 1494 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F--PDEKEFT----GAOSGGP
                                                                                                                                                                                                                               Local Similarity 35.19 les 71; Conservative
                                                                                                                                                        320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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                                                                                                                                                           Sequence
                                                                                                                                                                                                          Query Match
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TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQP

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WO200153312-A1.
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09-JUL-2000;
19-JUL-2000;
                                                                                    Homo sapiens.
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19-OCT-2000;
                                                                                                                                                                                                                                               21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                 26-JUL-2001
                                            leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
Wang J, W
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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    NAMES OF COLOR OF STREET STREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIPAPAPKPAAPPRPLDRESP--GVENKLIP-SVGSPASSTPLPPDGTGPNSTPNNRAVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVSQGSNSSSADPKA--PPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRML 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene mouse beta-catenin nuclear localisations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a beta-catenin nuclear localised protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 232.5; DB 23; Length
35.1%; Pred. No. 2.7e-08;
Live 23; Mismatches 75; Indels
                                                                                beta-catenin nuclear localised protein; cancer;
                                      Mouse beta-catenin nuclear localised protein.
                                                                                                     gene therapy; EST; expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 81-88; 113pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 F--PDEKEFT----GAQSGGP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 LRSGETEPFLKGPPGGAGEGGP 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide SEQ ID NO 2286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM39141 standard; Protein; 707
                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                19-SEP-2001; 2001WO-JP08140
                                                                                                                                                                                                                                                                                                      22-SEP-2000; 2000JP-0287876
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       Akiyama T, Adachi S;
                                                                                                                                                                                                                                                                                                                                                                                                                             2002-330014/36.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-330014,
N-PSDB; ABK47631
                                                                                                                                                                               WO200224738-A1
                                                                                                                                             Mus musculus.
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02-JUL-2002
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                                                                                Mouse;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification.
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amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 16.3%; Score 167.5; DB : Local Similarity 40.0%; Pred. No. 0.00053.
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Xu C, Xue AJ,
R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Asundi V, Chw
Wang Z, Wehrman T, X,
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||| | ||| | |
163 GAPPTPPSSGVPTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
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N-PSDB; AAI58297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.N.S disorders.
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13-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 SLPPPPPPRSNAAGSIPLPPQGRSAPPPPPRSAPSTGRQPPPLSSSRAVSNPPAPPPA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for identifying modulators of actin polymerisation. The method involves using proteins that contain at least one binding motif for proteins of the Enay TASP (vasodilator-stimulated phosphoprotein) family in the preparation of reagents for identification/screening of molecules that modulate formation of the actin cytoskeleton. The proteins used in the method bind to the Arp2/3 protein omplex. The modulators identified by the method are potentially useful for treating disorders of actin polymerisation, e.g. metastatic cancer or parasitic infection; and as cytotoxic agents. The present sequence one such protein with binding motif(s) for Ena/VASP proteins, which was used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 IQNISNNKTERSTA-----PLNTQISA----LRNDPKPLPQQPPAPANQDQ----NSSQNT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulators of actin polymerization, potentially useful for treating tumor metastasis and parasitic infection, using proteins that
                                                                                                                                                                         Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein; metastatic cancer; parasitic infection; cytotoxic; WASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Noireaux V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louvard D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%; Score 162.5; DB 30.9%; Pred. No. 0.00097, tive 21; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golsteyn RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Pages 107-109; 109pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG67370 standard; Protein; 574 AA.
  574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contain Ena/VASp binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fradelizi J, Friederich E,
                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001WO-FR00843.
AAM52322 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                 2000FR-0003637
                                                                                     (first entry)
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                                                                                                                                                                                                                                        Schizosaccharomyces pombe
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                                                                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention
                                                                                                                                                                                                                                                                                WO200171356-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURI-) INST
                                                                                                                           WASP homolog
                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2000;
                                                                                     18-JAN-2002
                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                          AAM52322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sykes
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Matches
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AAG67370
ID AAG6
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AC AAG6
  NAMES OF COLOR OF STREET STREE
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55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein) homologue. Peptide fragments of Wash-family proteins of but and of the colls are used to prepare reagents for detecting compounds that inhibit or stimulate formation of the actin cytoskeleton, and thus inhibit or stimulate cell motility. The peptides are used to detect and identify compounds which are potentially useful for treating diseases associated with dysfunction of actin polymerisation, particularly metastatic cancer and parasite infection; as cytocoxic agents for inhibiting/stimulating formation of the actin cytoskeleton and for detecting side-effects, on actin polymerisation, of pharmaceuticals. By modulating actin polymerisation, of pharmaceuticals. By modulating actin polymerisation, these compounds affect cell motility, embryonic development, the immune response and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fragments of WASP family proteins, useful for detecting and identifying modulators of actin cytoskeleton formation, potential anticancer and antiparasitic agents
                                                             Wiskott-Aldrich syndrome protein; WASP; actin cytoskeleton; cell motility; actin polymerisation; cancer; parasite infection; embryonic development; immune response; wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Golsteyn RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a WASP (Wiskott-Aldrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 162.5; DB 22;
Pred. No. 0.00097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Noireaux V, Prost J, Sykes C, Friederich E,
Louvard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG27250 standard; Protein; 406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Scoi
30.9%; Pred
itive 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Fig 8; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-2000; 2000WO-FR03569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99FR-0015900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCI.
                                                                                                                                                                                           Schizosaccharomyces pombe
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Matches 50; Conservative
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                                                                                                                                                                                                                                                            WO200144292-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURI ) CENT
(CURI - ) INST
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Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNa methodologies \,
                                                                                                                       Human mammary carcinoma-derived DKFZphmcf1_1c23 homologue #15.
                                                                                                                                                     Human; gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example III; Page 551; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                      (GEHU-) GERMAN HUMAN GENOME PROJECT.
                               ABU52945 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                          18-AUG-2000; 2000WO-IB01496.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-327840/34.
                                                                                                                                                                                                                WO200112659-A2.
                                                                                                                                                                                                                                                                                                        18-AUG-1999;
                                                                                                                                                                                                                                                                                                                        28-SEP-1999;
                                                                                         14-APR-2003
                                                                                                                                                                                                                                              22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                    Wiemann S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymersae chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 N-KLIPSVGSPASSTPLPPDGTGPNSTP-NNRAVTPVSQGSNSSSADPKAPPPPVSSGE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 PKPLPQOPPAPA----NQDQNSSQNTRLQPTPPIPAPAPKPA-APPRPLDRESPGVE 84
                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity .
                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.5%; Score 159; DB 22; Length 40
32.0%; Pred. No. 0.0012;
live 15; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 57609; 103pp; English.
                            Novel human diagnostic protein #27241.
                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217.23-AUG-2000; 2000US-0649167.
 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPSPSPSP 147
                                                                                                                                                                                                                                                                                                                                   2001-639362/73
                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 AA;
                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS91437
                                                                                                                                  WO200175067-A2.
                                                                                                      Homo sapiens.
 18-FEB-2002
                                                                                                                                                                                                                                                                                                       Drmanac RT,
                                                                                                                                                                11-0CT-2001
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99US-0149499,

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This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P----AAPPRPLDRESPGVENKLIPSVGSPASSTPLP---PDGTGPNSTPNNRAVTPV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 PPPVKSPPPPAPVSSPPPVKS---PPPPAPVSSPPPPVKSPPPPAPISSPPPVKSPP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KTERSTAPLNTQISALRNDPKPLP--QQPPAPANQDQNSSQNTRLQP----TPPIPAPAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human mammary carcinoma-derived DKF2phmcf1_1c23 homologue #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               15.4%; Score 158.5; DB 32.0%; Pred. No. 0.00082; tive 17; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPAPVSSPPPPVKSPPPPAPVSSPPPPIKSPPP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGSNSSSADP-KAPPPP-PVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU52939 standard; Protein; 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                      256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-2003
                                                                                                                                                                                                                                                                                                                                                                      Seguence
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interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1998
                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW37151;
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW37151
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                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                            This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-----AAPPRPLDRESPGVENKLIPSVGSPASSTPLP---PDGTGPNSTPNNRAVTPV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                          14 KTERSTAPLNTQISALRNDPKPLP--QQPPAPANQDQNSSQNTRLQP----TPPIPAPAPK 68
                                                                                                                                                                                                          Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                  15.4%; Score 158.5; DB 22; Length 270; 32.0%; Pred. No. 0.00087;
         Human; gene therapy; vaccine; disease treatment; detection,
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 36981.
                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 PPAPVSSPPPPVKSPPPPAPVSSPPPPIKSPPP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 SQGSNSSSADP-KAPPPP-PVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                           Example III; Page 550; 1095pp; English
                                                                                                                                              (GEHU-) GERMAN HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB70063 standard; Protein; 446
                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                          18-AUG-2000; 2000WO-IB01496
                                                                                                               99US-0149499
99US-0156503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                     WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                             270 AA;
                                                  WO200112659-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical
                               Homo sapiens.
                                                                                                               18-AUG-1999;
                                                                                                                         28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                       22-FEB-2001
                                                                                                                                                                  Wiemann S;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB70063;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
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91 VG------SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention isseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3611), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL01840-ABL16175) and the encoded proteins in sequence at a for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPA--PKPAAPPRPLDRESPGVENKLIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neural Mena+ protein; mammalian Ena; Enabled protein; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ 1D NO 36981; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 158.5; DB 22; Length
29.6%; Pred. No. 0.0014;
Live 11; Mismatches 64; Indels
                                                                                                                                                                                                                                 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by GGN"
                                                                                                                                                                                                                                    Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key Location/Qualifiers
Misc-difference 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 SGEPPTLGENPDGLSQEGLEHR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW37151 standard; Protein; 783 AA.
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PPSPPSPQPGPEYLPPDQPKPR
                                                                                                                                                                                                                                 Li PWD,
23-MAR-2001; 2001WO-US09231
                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse neural Mena+ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75
                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 AA;
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RESULT 15
AAW37153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PSVGSPASS-TPLPPD-GTGPNSTPNNRAV- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 LSHCGSQASPPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGDSSASEPGLQAAS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                This protein comprises novel murine neural Mena+. Its amino acid sequence was deduced from a CDNA clone (see AAV02998) obtained from a mouse brain cDNA ilbrary. Neural Mena+ contains an exon that introduces 244 amino acids between amino acids 238 and 239 of mammalian Ena (Mena, see AAW37148). Two other isoforms, neural mammalian Ena (Mena, neural Mena++ (see AAW37153), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural mena+ (see ABW37181) are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and Evl canes of the acid of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 KPLPQQPPAPANQDQN-----SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                             Detection of modulators of Mena and Bna-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + protein; mammalian Ena; Enabled protein; Ev1 protein; cell morphology; cell adhesion; cell differentiation; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.4%; Score 158; DB 19; Length 783; 26.3%; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 QPAESPTPQG--LVLGPPAPPPPPLPSGPAYASALPPPPGPPP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QISALRNDP--
                                                                                                                                           Soriano P, Wehland J;
                                                                                 (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.00
15; Mismatches
                                                                                                                                                                                                                                                                                                                Example 4; Page 58-60; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW37152 standard; Protein; 787 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DRESPGVENKLI----
                                                  96US-0675815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse neural Mena++ protein.
              97WO-US11669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.4 Best Local Similarity 26.3 Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 NKTERSTAPLNT---
                                                                                                                                         Niebuhr K,
                                                                                                                                                                         WPI; 1998-101197/09.
N-PSDB; AAV02998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           783 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mena++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytoskeleton;
              03-JUL-1997;
                                                05-JUL-1996;
                                                                                                                                       Gertler FB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
\delta
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----DRESPGVENKLI------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 LSHCGSQASPPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGDSSASEPGLQAAS 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 SPVPQMPPSPTAPNGSLDSVTYPVSPPPPSGPAAPPPPPPPPPPPPPPPPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 KPLPQQPPAPANQDQN-----SSQNTRLQPTPPIPAPAPKPAAPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a cDNA clone obtained from a mouse brain cDNA library. Two other isoforms, neural Mena+ (see AAW37151) and neural Mena+++ (see AAW37153), are also disclosed. Unlike mammalian tissue-specific distribution. Based on the disclosed Mena and Evl genes (see also AAW37148), and proteins (see also AAW37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TPVSQGSNSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPAESPIPQG--LVLGPPAPPPPPLPSGPAYASALPPPFGPP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 158; DB 19; 26.3%; Pred. No. 0.0028; ive 15; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                      Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QISALRNDP-
                                                                                                                                                                                                                                                                  (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 60-63; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                      Soriano P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW37153 standard; Protein; 802 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse neural Mena+++ protein.
                                                                                                                                                                                                             96US-0675815.
                                                                                                                                                          97WO-US11669
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                                                                                                                                                                                                                                                                                                                                                 Gertler FB, Niebuhr K,
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-101197/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    787 AA;
Mus musculus.
                                            WO9801755-A1
                                                                                                                                                     03-JUL-1997;
                                                                                                                                                                                                             05-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 SPVPQMPPSPTAPNGSLDSVTYPVSPPPTSGPAAPPPPPPPPPPPPPPPPPPPLAPLAS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 NKTERSTAPLNT------33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 KPLPQQPPAPANQDQN-----SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein comprises novel murine neural Mena+++. Its amino acid sequence was deduced from a cDNA clone obtained from a mouse brain cDNA library. Two other isoforms, neural Mena+ (see AAW37151) and neural Mena+ (see AAW37152), are also disclosed. Unlike mammalian Ena (Mena, see AAW37140), neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and Evl genes (see also AAW72996-98) and proteins (see also AAW37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control
Neural Mena+++ protein; mammalian Ena; Enabled protein; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. Rethod of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 QPAESPTPQG--LVLGPPAPPPPPPPPSGPAYASALPPPPGPPP 569
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                                                                                                                                                                                                                                                                                                                                   Soriano P, Wehland J;
                                                                                                                                                                                                                                                                         (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 63-65; 77pp; English.
                                                                                                                                                                                                 97WO-US11669.
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Best Local Similarity
Matches 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation
                                                                              Mus musculus
                                                                                                                  WO9801755-A1
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Search completed: October 15, 2003, 10:30:25 Job time: 120.268 secs

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Sequence 12, Appli
Sequence 7, Appli
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Sequence 32, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 53, Appli
Sequence 54, Appli
Sequence 64, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 74, Appli
Sequence 14, Appli
Sequence 74, Appli
Sequence 58, Appli
Sequence 74, Appli
Sequence 58, Appli
                                                                   October 15, 2003, 10:27:32; Search time 39.2529 Seconds (without alignments) 209.113 Million cell updates/sec
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1028
1 TIVSFHIQNISNNKTERSTA......LFPDEKEFTGAQSGGPQONP 194
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-952-800-2
US-08-764-870-7
US-08-980-115-7
US-07-952-800-4
US-08-580-6800-4
US-08-580-580-6
US-09-262-653A-6
US-09-262-653A-6
US-09-262-91A-24873
US-09-081-97-2
US-09-081-91-11-53
US-08-818-111-53
US-08-818-111-53
US-09-056-556-53
US-09-056-556-53
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US-07-757-022B-42
US-07-757-022B-142
US-07-757-022B-50
US-07-757-022B-46
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S-07-757-022B-58
S-07-757-022B-104
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                                                                                                                                                                                                       328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                      length: 0
length: 2000000000
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Match Length DB
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120.5
149.5
149.5
1143.5
138.5
138.5
136.5
136.5
136.5
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Maximum DB s
                                                                                                                                             Sednence:
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                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.
                                                                                                                    Title:
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Sequence 60, Appl Sequence 48, Appl Sequence 52, Appl Sequence 2, Appl Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli	of Hermans xes and HPS	4; Length 816; 5; 64; Indels 43; Gaps 7; PPAPANQDONSSQNTRLQPTPPIP 63
US-07-757-022B-60 US-07-757-022B-48 US-07-757-022B-52 US-07-757-022B-52 US-07-757-022B-62 US-08-995-53 US-08-217-327-4 520236-37 US-08-214-247A-10 US-09-514-247A-10 US-09-312-258-3 US-09-313-258-3 US-09-313-528-3 US-09-313-528-3 US-09-913-528-3 US-09-599-366-3	GNMENTS aracterizatio Protein Compl teins 6,225D	Score 161.5; DB Pred. No. 1.6e-0 7; Mismatches LPQQ I TFTPVQPTSPPPGPVAQVENKLIPS QIATSTSLLAAQSLVPP VQGSNSSADPKAPPP 1 -QQLSKSQVEDPL EMBER OF THE NUCL R SUPERFAMILY AND OWNSEND
3.0 1320 33.0 13554 33.0 13631 33.0 13631 33.0 13631 33.0 1404 4404 22.9 2145 22.8 2145 22.7 325 22.7 325 22.7 325 22.7 325 22.7 325 22.7 325 22.7 325 23.7 325 23.8 325	ation US/ : lan, Kris lan, Kris ore, Step ev, Veltz : Isolati : Syndro : Syndro : Intere 966-523 b6-523 Ver. 2.1 plens	imilarity 32.1%; Score ; Conservative 7; Mis RSTAPLNTQISALRNDFRPLP RPAAPALTSVPAPPAPTPTPTPVQP RPAAPPRPLDRESPG RPAAPHTGPPGPIPVPAPPTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT
133.5 133.5 133.5 133.5 133.5 133.5 133.5 133.5 133.5 130.5 130.5 130.5 130.5 130.5 130.5 130.5		Ch 117 177 777 777 777 64 99 99 11NF 99 97 97 97 97 97 97 97 98 97 97 97 97 97 97 97 97 97 97 97 97 97
20000000000000000000000000000000000000	RESULT 1 US-09-266-7 Sequence Patent w GENERAL APPLICAL APPLICAL TITLE O) TITLE O) TITLE O) TITLE O) TITLE OO T	Query Mat Best Loca Matches Qy Db Sy QY Db 6 Qy Db 6 Qy 1 Db 6 Qy 1 Db 6 Qy 1 THEEUT 2 US-07-952-8 Sequence Sequence Patent No TITLE

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NAME: NAKAMULA, JACKIE N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAWE: Nabening Tackion
                                                            APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 525 amino acids
TYPE: amino acid
STRANDEDNESS:
                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-764-870-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 -PPPPVSSG 141
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US-08-980-115-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S
APPLICANT: Baxter, John D
APPLICANT: Hetterick, Robert J
APPLICANT: Wagner, Richard L
APPLICANT: Wagner, Richard L
APPLICANT: Manner, Peter J
APPLICANT: Washietti, James W
APPLICANT: West, Brian
ITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
TITLE OF INVENTION: Binding Domains
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUDRESSEE: Cooley Godward
STREET: Five Palo Alto Square, 3000 El Camino Real
STREET: CA
                                                                                                        COMPUTER READABLE FORM;
MEDIUM TYPE: Rioppy disk
COMPUTER: IRM PC Compatible
COMPOTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,800
FLING DATE: 19920928
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 15280-21-1
RELEPHONE: 415-543-5600
TELLEPHONE: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACID
STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
CITY: SAN FRANCISCO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.6%; Score 150.5; DB
Best Local Similarity 31.0%; Pred. No. 7.7e-05,
Matches 40; Conservative 11; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-07-952-800-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 -PPPPVSSG 141
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|191 CPPPGGPG 199
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OPERATING SYSTEM:
                                                                                               USA
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                                                                                               COUNTRY:
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Sequence 7, Application US/08980115

Sequence 7, Application US/08980115

Sequence 7, Application US/08980115

GENERAL INFORMATION:

APPLICANT: Scanlan Thomas S.

APPLICANT: Baxter, John D.

APPLICANT: Rather, Peter J.

APPLICANT: Washner, Peter J.

APPLICANT: Washner, Peter J.

APPLICANT: Application, John D.

APPLICANT: Application, John D.

APPLICANT: Applicant: Washner, Peter J.

APPLICANT: Applicant: Washner, Washner, Washner, Peter J.

APPLICANT: Applicant: Washner, Was
                                                                                                                                                                                                                                                                                                                                           78 SSPNPLPQGVPPPSPPG-----PPLPPSTAPTLGGSGAPPPPPMPPPPLGSPFP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP---- 133
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                                                                                                                                                   33;
                                   Length 525;
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Query Match 14.5%; Score 149.5; DB 3; Best Local Similarity 31.0%; Pred. No. 9.1e-05; Matches 40; Conservative 10; Mismatches 46;
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                                                                                                                                                                                                                                                       127 VISS ---- SMGSPGLPPPAPPGFSGPVSSPQINSTVSLPGGGSGPPEDVKPPVLGVRGLH 182
                                                                                                                                                                                                                                   31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-----PKPAAPPRPLDRESP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPANDLSQGIRPSSP------PGPPLTPSAPPPMMPPPPLGSPFVISS---51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OZATO, KEIKO
TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMONE
TITLE OF INVENTION: RECEPTOR SUPERFAMILY AND A CDNA CLONE THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND AND TOWNSEND
STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                          82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP --
                                                                                                                                                               Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 446;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/952,800
FILING DATE: 19920928
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-21-1
                                                                                                                                                           14.5%; Score 149.5; DB 3; 31.0%; Pred. No. 9.1e-05; tive 10; Mismatches 46;
                                                FEATURE: NAME/KEY: DOMAIN

LOCATION: (292)..(523)

CTHER INFORMATION: minimal ligand binding domain
US-08-980-115-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 143.5; DB 1
30.3%; Pred. No. 0.00023;
tive 12; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/07952800 Patent No. 5403925 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                    Query Match
Best Local Similarity 31.0%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 446 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                             134 -PPPPVSSG 141
                                                                                                                                                                                                                                                                                                                                                                                                                 183 CPPPGGPG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAN FRANCISCO
               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94105
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LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-952-800-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-952-800-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: S
STATE:
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Best Local
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APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: PORTIONS AND PRODUCTS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ANDRESSONDER ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5961 EKTTAEKKAELEKAEADLKKAVDEPETPAPAPAPAPAPA-------PTPEAPAP 6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- 6055
                         64 APAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ERSTAPLNTQISALRND------PKPLPQQPPAPANQDQNSSQNTRLQPTP--PIP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6008 АРАРКРАРАРКРАРАРКРАРАРКРАРАРКРАРАРКРАРАРКРАРАРАРКР-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 140.5; DB 4; Length 8991;
Pred. No. 0.014;
9; Mismatches 62; Indels 43;
89 PSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUFTWARE: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILLNG DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 NSSSADPKAPPPPVSSGEPPTLGENPD----GLSQE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Curtis, Morris & Safford, P.C.
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                           Sequence 32, Application US/08714741
Patent No. 6500613
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6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.78; 27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 8991 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                     140 SG 141
                                                                                                                            111 PG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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COTTON FIBER TISSUE-SPECIFIC GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 PPPPVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 APTPPYMPPTPPTKAPTP 190
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.2%;
Matches 43; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 297 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-262-653A-6
        TITLE OF INVENTION: CO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                          STREET: but
                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTR: United ZIP: 94111-4187
                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                             20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-819-013-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 TPPXKPPAP------APPTKAPTPP-FKPPAPAPPTKAPTRPPKKPTAPAPPVK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPI--PAPAPKPAAP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                     APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Kolchi, Fulisawa
APPLICANT: Susmu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
APPLICANT: Randy, Allen
TITLE OF INTENTION: COTTON FIBER TISSUE-SPECIFIC GENES
  6056 --APAPAPAPAPKPEKPAEKPAPAPKPETPKTGWKQE 6090
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPOTED:
COMPUTER: TBM PC COMPOTED:
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/580,545B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.5%; Score 138.5; DB 2; Best Local Similarity 31.2%; Pred. No. 0.00038; Matches 43; Conservative 9; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bretschoeider, Barry E.
REGISTRATION UNBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/068001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202/783-5070
TELEFRA: 202/783-5331
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 601 Thirteenth Street, NW
                                                                                              Sequence 6, Application US/08580545B
Patent No. 5932713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. CONTROL SENERAL INFORMATION:
APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Koichi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
APPLICANT: Randy, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09262653A
Patent No. 6166294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 PPPPPVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 2027/183-202.
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
1.ENGTH: 297 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                  CITY: Was
STATE: DC
                                                                          US-08-580-545B-6
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US-09-262-653A-6
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73 PRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPI--PAPAPKPAAP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 138.5; DB 3;
Pred. No. 0.00038;
9; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 17-MARE: US/08/819,013
FILLING DATE: 17-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Flehr, Hohbach, Test, Albritton & STREET: Four Embarcadero Center, Suite 3400 SITY: San Francisco SITY: San Francisco SITY: California COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/068001
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202/783-5070
TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
ADDRESSEE: Fish & Richardson P.C. STREET: 601 Thirteenth Street, NW
                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chan, Andrew C.
TILLE OF INVENTION: BLINK PROFEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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81 -PGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 PLPQQ-----PPAAPANQDQNSSQNTRLQPTPPIPAPAPKPA----APPRPLDRES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 136.5; DB 2; Length 1248;
Pred. No. 0.0029;
8; Mismatches 59; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
                                                                                   120 SQGSNSSSADPKAPPPPVSSGEPPTLGENPDG 152
                                                                                                                              ------PPVPPSPPPS--PPPVPPSPPG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: SCIENCE & TECHNOLOGY LAW GROUP: 75 DEN'SE DRIVE HILLSBOROUGH
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      Sequence 2, Application US/09080897
Patent No. 5985574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09323735; Patent No. 6197932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UNTELECOMMUNICATION INFORMATION: TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (650) 343-434
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: ;
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 SGEPPTLGENPDG 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-323-735-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-09-080-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                              107
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 IDNRSSQRHSPPFS------KTLPSKPSWP------SEKARLTSTLPALTALQKP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 AAPPRP---LDRESPGV-----ENKLIPSVGS--PASSTPLPPDGTGPNSTPNNRAVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 QVPPKPKGLLEDEADYVVPVEDNDENYIHPTESSSPPPEKAPMVNRSTKPNSS----T 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 PVS-----QGSNSSSADPKAPPP----PPVSSGEPPTL-------GENPDGLSQEQ-- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PPIPAAPAKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 IQNISNNKTERSTAPL-----NTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 VQAFCSDSSKPGTLSLPNGLFFTNAQLSSLQPPCKPVP----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.3%; Score 137; DB 2; Length 456 Best Local Similarity 25.9%; Pred. No. 0.00083; Matches 51; Conservative 26; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TELING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: S11Va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REPERENCE/DOCKET NUMBER: 38,304
REPERENCE/DOCKET NUMBER: 38,304
REPERENCE/DOCKET NUMBER: 38,304
REPERENCE (415) 781-1989
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 136.5; DB 4; 26.8%; Pred. No. 0.00023; Live 19; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24873, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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277 PAERHRGSSHRQEAVQS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 -----LEHRERSLQT 167
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                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
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Matches 41; Conserv
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US-09-252-991A-24873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 PPLPEGVGIPSPSSLPGGTAIPP----PPPLPGSARIPPPPPLPGSAGIPPPPLPGE 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 PLPQQ-----PPAPANQDQNSSQNTRLQPTPPIPAPAPKPA----APPRPLDRES----- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 136.5; DB 3; Length 1248; 32.3%; Pred. No. 0.0029; tive 8; Mismatches 59; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                         ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA COUNTRY: USA
APPLICANT: King, Mary-Claire
APPLICANT: Lych, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Melcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
CORPREDORMENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UW97-001
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Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTATION UNDRER: 36,627
REFERENCE/DOCKET UNDRER: UW97-
TELECOMMUNICATION INFORMATION:
TELEFONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antoni
APPLICANT: Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1248 amino acids
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Best Local Similarity 32...
hes 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   94010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-818-112-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-323-735-2
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 HMHOVDPNLTRRKGRLAALAIAAMAS-ASLVTVAVPATANADP-----EPAPPVPTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardick, Thomas S.
APPLICANT: Twardik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.1%; Score 135; DB 3; Length 332; Best Local Similarity 27.6%; Pred. No. 0.00084; Matches 42; Conservative 15; Mismatches 57; Indels
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS NUMBER OF SEQUENCES: 153 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
       ...urwSSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GSNSSSADPKAPPPPVSSGEP-PTLGENPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 NAAPPPADPNAPPPPVIAPNAPQPVRIDNPVG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210121.41106
                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/818,112
13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-MAR-CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-818-111-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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66 APKP----AAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQ 121
                                                                                                                                                                                                                                                                                  6 HIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAP 65
                                                                                                                                                                                                                                                                                                                           7 HMHQVDPNLTRRKGRLAALAIAAMAS-ASLVTVAVPATANADP------EPAPPVPTT 57
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                           38;
                                                                                                                                                                                      Query Match 13.1%; Score 135; DB 4; Length 332; Best Local Similarity 27.6%; Pred. No. 0.00084; Matches 42; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GSNSSSADPKAPPPPVSSGEP-PTLGENPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: October 15, 2003, 10:32:01 Job time: 40.2529 secs
                                    ; LENGTH: 332 amino acids; TYPE: amino acid a STRANDEDNESS: single; TOPOLGGY: linear
                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 HIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAP 65
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7 HMHQVDPNLTRRKGRLAALAIAAMAS-ASLVTVAVPATANADP-----EPAPPVPTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Skedy Yaair A.W.
APPLICANT: Skelky, Yaair A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.1%; Score 135; DB 4; Length 332; Best Local Similarity 27.6%; Pred. No. 0.00084; Matches 42; Conservative 15; Mismatches 57; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C6
TELEPROME: (206) 622-4900
TELEPROME: (206) 622-4900
TELEPROME: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTER STICS:
LENGTH: 332 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GSNSSSADPKAPPPPVSSGEP-PTLGENPDG 152
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPRA: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JMBER: US/09/056,556
07-APR-1998
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linear
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US-09-056-556-53
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                   OM protein - protein search, using sw model
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October 15, 2003, 10:32:06; Search time 82.2802 Seconds (without alignments) 379.908 Million cell updates/sec Run on:

1 TIVSFHIQNISNNKTERSTA........LFPDEKEFTGAQSGGPQQNP 194 US-09-915-543-15_COPY_199_392 1028 Perfect score: Sequence: Title:

BLOSUM62 Scoring table:

600653 seqs, 161128416 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1. (cgn2_6/ptodata_1/pubpaa_US07_PUBCOMB.pep:*
2. (cgn2_6/ptodata_1/pubpaa_US07_PUBCOMB.pep:*
3. (cgn2_6/ptodata_1/pubpaa_US06_BUBN_PUB.pep:*
3. (cgn2_6/ptodata_1/pubpaa_US06_PUBCOMB.pep:*
4. (cgn2_6/ptodata_1/pubpaa_US06_PUBCOMB.pep:*
5. (cgn2_6/ptodata_1/pubpaa_US07_NEW_PUB.pep:*
6. (cgn2_6/ptodata_1/pubpaa_US08_NEW_PUB.pep:*
7. (cgn2_6/ptodata_1/pubpaa_US08_NEW_PUB.pep:*
8. (cgn2_6/ptodata_1/pubpaa_US09_PUBCOMB.pep:*
9. (cgn2_6/ptodata_1/pubpaa_US09_PUBCOMB.pep:*
10. (cgn2_6/ptodata_1/pubpaa_US09_PUBCOMB.pep:*
11. (cgn2_6/ptodata_1/pubpaa_US09_PUBCOMB.pep:*
12. (cgn2_6/ptodata_1/pubpaa_US09_PUBCOMB.pep:*
13. (cgn2_6/ptodata_1/pubpaa_US100_PUBCOMB.pep:*
14. (cgn2_6/ptodata_1/pubpaa_US100_PUBCOMB.pep:*
15. (cgn2_6/ptodata_1/pubpaa_US100_PUBCOMB.pep:*
16. (cgn2_6/ptodata_1/pubpaa_US10_PUBCOMB.pep:*
17. (cgn2_6/ptodata_1/pubpaa_US10_PUBCOMB.pep:*
18. (cgn2_6/ptodata_1/pubpaa_US10_PUBCOMB.pep:*
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18. (cgn2_6/ptodata_1/pubpaa_USS10_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 15, Appl	Sequence 5. Appli	Sequence 278. App	Sequence 76. Appl	Segmence 38. Appl	Segmence 2. Appli	Sequence 17. Appl	Seguence 86. Appl	Seguence 2. Appli	Seguence 2. Appli	Sequence 2. Appli	Sequence 1068. Ap	Sequence 1068. Ap	Sequence 1068. Ap	Sequence 24, Appl	
SUMMARIES	ID	US-10-322-579-15	US-10-322-579-5	US-09-919-039-278	US-10-168-097A-76	US-10-239-431A-38	US-09-823-240-2	US-10-086-464-17	US-10-021-660-86	US-10-078-547-2	US-09-922-226-2	US-10-098-184-2	US-09-922-217-1068	US-09-833-263-1068	US-10-025-380-1068	US-10-078-547-24	
	DB	15	15	11	12	12	6	14	12	14	11	15	0	10	14	14	
	Query Match Length DB	1426	35	707	574	574	802	731	509	503	533	533	5179	5179	5179	507	
ď	Query	100.0	17.3	16.3	15.8	15.8	15.4	15.0	14.8	14.7	14.6	14.6	14.6	14.6	14.6	14.5	
	Score	1028	178	167.5	162.5	162.5	158	154.5	152	151.5	150.5	150.5	150	150	150	149	
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i Lack o opposition	Segmence 22 April			Sequence 5. Appli	Sequence 282. App	Sequence 12 Appl	Sequence 32 Appl	Sequence 70. Appl	Sequence 70. Appl	Segmence 640 App	Sequence 56. Appl	Sequence 36 Appl	Sequence 46. April		Sequence 4 Appli				Sequence 4, Appli	Sequence 1902, ap	Sequence 37. Appl	Segmence 53. April		7	7007	100	,,,		Sequence 1, Appli
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731 14 US-10-086-464-8	12	12	15	14	15	12	12	σ	7	H	H	H	=======================================	1	÷;	15	14	7		633 12 US-10-168-097A-66	13	12	13	12	σ	5	12	12	11
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148.5	144.5	144.5	144.5	142.5	141.5	141.5	141.5	141	141	141	139.5	139.5	139	139	139	138	137,5	137.5	136,5	136	136	135	135	135	134,5	134.5	134.5	134.5	134
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

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Sequence 15, Application US/1032579

Publication No. US20030114413A1

GENERAL INPORMATION:

APPLICANT: BASLER, Konrad

APPLICANT: BROBER, Erich

APPLICANT: REABES, Thomas

APPLICANT: KRAMPS, Thomas

APPLICANT: FREEENING DIVERTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH

TITLE OF INVENTION: THERAPEDITIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

FILE REFERENCE: 060361

CURRENT APPLICANTON NUMBER: US/09/915,543

PRIOR APPLICANTON NUMBER: 05/221,502

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 22

SOFFWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%; Score 1028; DB 15; Length 1426; Similarity 100.0%; Pred. No. 7.9e-59; 94; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human lgs/bcl9
US-10-322-579-15
US-10-322-579-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 15
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APPLICANT: FRADELIZE, JULIE
APPLICANT: FRADELIZE, JULIE
APPLICANT: FRADELIZE, JULIE
APPLICANT: GOLSTEYN, ROY M.
APPLICANT: GOLSTEYN, ROY M.
APPLICANT: LOUVARD, DANIEL
APPLICANT: LOUVARD, DANIEL
APPLICANT: SYKES, CECILE
TITLE OF INVENTION: PEPTIDE SEQUENCES COMPRISING ONE OR MORE UNITS BINDING
TITLE OF INVENTION: PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/10/239, 431A
CURRENT APPLICATION NUMBER: PCT/FR01/00843
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT-----SAPP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S3 QSGPKP-PIPPPPPHQQQQPPPQQPPPQQPPHQPPHPQPHQQQQPPPHQQSSKPVV 111
                                                                                                  84 EN--KLIPSVGS--PASSTPLP-----PDGTGPNSTPN-NRAVTPVSQGSNSSSADP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT 54
30 RNDPKPLPQQPPAPANQDQN--SSQNTRLQPTPPIPAPAPKP----AAPPRPLDRESPGV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 30.9%; Score 162.5; DB 12; Length 574; Similarity 30.9%; Pred. No. 0.0041; 50; Conservative 21; Mismatches 64; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                      Sequence 76, Application US/10168097A
Publication No. US20030166245A1
GENERAL INFORMATION:
APPLICANT: CENTRE NATIONAL OF THE RECHERCHE SCIENTIFIQUE
APPLICANT: INSTITUT CURIE
TITLE OF INVENTION: WASP FAMILY PROTEIN FRAGMENTS, AND USES THEREOF
FILE REFERENCE: IRPS99MASP
CURRENT APPLICATION NUMBER: US/10/168,097A
CURRENT PILING DATE: 2002-06-17
NUMBER OF SEQ 1D NOS: 84
NUMBER OF SEQ 1D NOS: 84
NUMBER OF SEQ 1D NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                   131 KAPPPPPVSSGEPPT 145
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163 GAPPPTPPSSGVPTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.8%
Best Local Similarity 30.9%
Matches 50; Conservative
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APPLICANT: BROWNER, Erich
APPLICANT: BROWNER, Erich
APPLICANT: BROWNER, Erich
APPLICANT: RAMES, Thomas
APPLICANT: REAMES, Thomas
APPLICANT: PETER, Oliver
ITILE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING
FILE REFERENCE: 060361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT APPLICATION NUMBER: US/09/915,543
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE: Kaser, Matthew R.

IITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 U3

CURRENT APPLICATION NUMBER: U5/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                          121 QGSNSSSADPKAPPPPVSSGEPPTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEK 180
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.3%; Score 167.5; DB 11; Length 707; 40.0%; Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20030108871A1 2457215CD1
US-09-919-039-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 17,3%; Score 178; DB 15; Best Local Similarity 100.0%; Pred. No. 2.4e-05; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 278, Application US/09919039 Publication No. US20030108871A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10322579 Publication No. US20030114413A1 GENERAL INFORMATION:
                                                                                                                             181 EFTGAQSGGPQQNP 194
                                                                                                                                                           379 EFTGAQSGGPQQNP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human lgs/bcl9
US-10-322-579-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                     RESULT 2
US-10-322-579-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 278
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LENGTH: 509
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                                                                                                                                                                55 RLQPTPP-----IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 ----DRESPGVENKLI------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV- 116
                                                                                                                                                                                                                                       408 SPVPQMPPSPTAPNGSLDSVTYPVSPPPTSGPAAPPPPPPPPPPPPPPPPPPPPPLAPPLAS 467
                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 LSHCGSQASPPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGDSSASEPGLQAAS 527
                                                                                                                                         7 IQNISNNKTERSTA-----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SSQNTRLQPTPPIPAPAPKPAAPPRPL-
                                                                                                        27;
                                                                        Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09823240

Patent No. US20020048813A1

GENERAL INFORMATION:
APPLICANT: Frank B. Gertler
APPLICANT: James E. Bear
APPLICANT: Jurgen Wehland
APPLICANT: Joseph Lourelo
TITLE OF INVENTION: Methods and Products for Regulating Cell
TITLE OF INVENTION: Methods and Products for Regulating Cell
TITLE OF INVENTION: Methods and CORRENT APPLICATION NUMBER: US/09/823,240

CURRENT APPLICATION NUMBER: US/09/823,240

PRIOR APPLICATION NUMBER: 60/194,564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10086464
Publication No. US20020199218A1
GENERAL INFORMATION:
APPLICANT: GORING, Daphne R. et al.
TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 158; DB 9; Length 802; llarity 26.3%; Pred. No. 0.011; Conservative 15; Mismatches 62; Indels
                                                       Score 162.5; DB 12; Leus-Pred. No. 0.0041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTL 146
                                                                                                                                                                                                                                                                                                        ---QISALRNDP--
                                                                   Query Match
15.8%; Score 162.5; I
Best Local Similarity 30.9%; Pred. No. 0.00
Matches 50; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
TYPE: PRT ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 NKTERSTAPLNT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus US-09-823-240-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 59; Conserv;
                                 US-10-239-431A-38
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US-10-086-464-17
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US-09-823-240-2
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Sequence 86, Application US/10021660

Publication No. US20030152926A1

GENERAL INFORMATION:

APPLICANT: Mutray, Richard

APPLICANT: Glynne, Richard

APPLICANT: Glynne, Richard

APPLICANT: Gos bicechnology, Inc.

APPLICANT: EOF INVENTION: No. US2003015226A1e1 Methods of Diagnosis of Anglogenesis,

TITLE OF INVENTION: Modilators

TITLE OF INVENTION: Modilators

TITLE OF INVENTION: Modilators

TITLE OF INVENTION: Modilators

FILE REFERENCE: 018501-0007100S

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: US/09/784,356

PRIOR APPLICATION NUMBER: US/09/784,356

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 135

SOFFWARE: FEASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- PPDGTGPNST-PNNRAVTPVSQG- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 TERSTAPLNTQISALRNDPKPLPQOPPAPANQDQNSSQNTRLQPTPPIPAPAPK--PAAP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 -----SNSSSADPKAPP-----PPPVSSGEPPTLGENPDGLSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 PSESTPPVNTASPPPPSPRRRSGPKPSFPPPINS-SPPNPSPNTPSLPE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
15.0%; Score 154.5; DB 14,
Best Local Similarity 27.6%; Pred. No. 0.017;
Matches 47; Conservative 20; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
14.8%; Score 152; DB 12;
Best Local Similarity 27.0%; Pred. No. 0.017;
Matches 60; Conservative 13; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 PRPLDRESPGVENKLIPSVGSPASSTPL----
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR APPLICATION NUMBER: US 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR PILING DATE: 2000-08-18
PRIOR PLICATION NUMBER: US 60/149,466
PRIOR FILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                     , URGANISM: Arabidopsis thaliana
US-10-086-464-17
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 731
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US-10-021-660-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 PPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAV--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 --TPVSQGSNSSSADPK-----APPPPPVSSGEPPTLGENPDGLSQEQLEHR-- 161
153 APPPPPPRSRAGSGAGALPCAGHTRRRRTSSPRSSPPLSGPPGRASPRGARPPPLLRAA 212
                                                  110 -TPNNRAVTPVSQGSNSSSADPKAPPPPVSSGE-----PP------TL-146
                                                                                12 NNK----TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNS-----SQNTRL-QPT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
14.7%; Score 151.5; DB 14; Length 503;
Best Local Similarity 26.5%; Pred, No. 0.019;
Matches 60; Conservative 25; Mismatches 84; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 FHPISDLPPPEPYVQTTKSYPSKLARNESR-SGSNRRERGGPPLPP 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 ------ERSLQTLRDIQRMLFPDEKEFTGA---QSGGPQQNP 194
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APPLICANT: Thacher, Scott M.
APPLICANT: Thacher, Scott M.
APPLICANT: Xiao, Jia-Hao
APPLICANT: Kusari, Jyolirmoy
APPLICANT: Chandraratna, Roshantha A.
TITLE OF INVENTION: Methods of Screening For Compounds That
TITLE OF INVENTION: Modulate Hormone Receptor Activity
                                                                                                                                                            147 GENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSG 188
                                                                                                                                                                                                           266 GSSPG-----PRRILIPLILRVGR-----PRSGAASG 291
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marayanaswamy Ramesh
APPLICANT: Marayanaswamy Ramesh
APPLICANT: Marayanaswamy Ramesh
APPLICANT: Inea M. Anton
APPLICANT: Inea M. Anton
APPLICANT: Raif S. Geha
TITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-005
CURRENT FILING DATE: 2002-02-19
PRIOR PILLATION NUMBER: 09/599.287
PRIOR APPLICATION NUMBER: 09/599.287
PRIOR APPLICATION NUMBER: 60/101.457
PRIOR APPLICATION NUMBER: 60/101.457
PRIOR FILING DATE: 1998-02-22
PRIOR FILING DATE: 1998-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10078547
Publication No. US20020199211A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
LENGTH: 503
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OTHER INFORMATION: Description of Artificial Sequence; No. US20030105333Ale - COTHER INFORMATION: synthetic construct US-10-098-184-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP----- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 SSPNPLPQGVPPPSPPG------PPLPPSTAPSLGGSGAPPPPPMPPPLGSFFP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAP----- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                         31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-----PKPAAPPKPLDRESP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA-----PKPAAPPRPLDRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                         Query Match 14.6%; Score 150.5; DB 11; Length 533; Best Local Similarity 31.0%; Pred. No. 0.023; Matches 40; Conservative 11; Mismatches 45; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 14.6%; Score 150.5; DB 15; Length 533; Similarity 31.0%; Pred. No. 0.023; 40; Conservative 11; Mismatches 45; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zapf, James W.
TITLE OF INVENTION: RRR ACTIVATING MOLECULES
CURRENT APPLICATION NUMBER: US/10/098,184
CURRENT FILLING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,342
PRIOR FILLING DATE: 2001-03-08
; FILE REFERENCE: P-AR 4681
; CURRENT APPLICATION NUMBER: US/09/922,226
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/284,797
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pfahl, Magnus
APPLICANT: Tachdisan, Catherine
APPLICANT: Al-Shamma, Hussien A.
APPLICANT: Fanjul, Andrea
APPLICANT: Pleynet, David P.M.
APPLICANT: Spruce, Lyle W.
APPLICANT: Fine, Richard
APPLICANT: Zapf, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10098184, Publication No. US20030105333A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-922-226-2
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Best Local Similarity
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SEQ ID NO 2
LENGTH: 533
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                                                                                                                                                                                                                                                 73 -----PRPLDRESPGVENKLIPSVGSPASSTPLPPDGT------GPNSTPNNR 114
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                                                                                                                        15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAP-- 72
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                                                                       Gaps
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14.6%; Score 150; DB 14; Length 5179;
Best Local Similarity 25.6%; Pred. No. 0.24;
Matches 41; Conservative 20; Mismatches 65; Indels 34
      Length 5179;
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILLIO DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
14.6%; Score 150; DB 10; Length 51
25.6%; Pred. No. 0.24;
.ive 20; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        115 AVTPVSQGSNSSSADPKAPP-----PPPVSSGEPPT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-025-380-1068; Sequence 1068, Application US/10025380; Publication No. US20020182191A1; GENERAL INFORMATION:
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Stolk, John A.
Wang, Tongtong
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Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
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APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
Query Match
Best Local Similarity 25.6%
Matches 41; Conservative
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US-10-025-380-1068
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US-10-078-547-24
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APPLICANT:
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APPLICANT:
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121, 471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 5179
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILIG DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
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Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
                                                                                                                                                                             Sequence 1068, Application US/09922217
Patent No. US20020076414A1
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Stolk, John A.
Wang, Tongtong
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Smith, Carole Lynn
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Secrist, Heather
Benson, Darin R.
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Best Local Similarity 25.68
Matches 41; Conservative
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Wang, Aijun
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191 CPPPGGPG 199
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US-09-833-263-1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 ---TPVSQGSNSSSADPK-----APPPPPVSSGEPPTLGENPDGLSQEQLEHR- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 TPQLPSRSGYDSPRSGPRPPLPPDRRSAGAPPPPPSTSIRNGFQDSP---CEDEWESRF 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 NNK-----TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNS-----SQNTRL-QPT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.9%; Pred. No. 0.027;
Matches 61; Conservative 25; Mismatches 83; Indels 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Translated WIP ORF NO. US20020199211A1 3 US-10-078-547-24
APPLICANT: Narayanaswamy Ramesh
APPLICANT: Miguel A. de la Fuente
APPLICANT: Ines M. Anton
APPLICANT: Eaif S. Geha
ITILE OF INVENTION: WIP, A WASP-ASSOCIATED
ITILE OF INVENTION: WIP, A WASP-ASSOCIATED
FILE REPERENCE: 1242-1022-025
CURRENT APPLICATION NUMBER: US/10/078,547
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR APPLICATION NUMBER: 60/10
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Search completed: October 15, 2003, 10:50:59 Job time : 83.2802 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 15, 2003, 10:27:32; Search time 46.0467 Seconds (without alignments) 405.170 Million cell updates/sec Run on:

US-09-915-543-15_COPX_199_392 1028 Perfect score: Title:

1 TIVSFHIQNISNNKTERSTA......LFPDEKEFTGAQSGGPQQNP 194

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sednence:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hvbothetical nrote	hypothetical prote	PTB-associated spl	Wiskott-Aldrich sv		=	- 02		hypothetical prote	extensin-like prot	extensin - Volvox	proline-rich prote	hypothetical prote		extensin-like prot	salivary proline-r	retinoid X recepto	mucin 2 precursor,	proline-rich prote	hypothetical prote	pistil extensin-li	unknown protein (i	prpL2 protein - hu	hypothetical prote	С	hypothetical prote	U.	hypothetical prote	
SUMMARIES	ID	S50755	T49801	A46302	T43556	T38819	T18535	B56708	F75518	S50754	S49915	S22697	S16748	T04455	T05441	D85257	PIHUPF	S37781	A43932	D29149	T32711	JQ1696	G86441	S52796	B86369	OZZQBK	T34279	P00479	D96711	
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d	Query Match	, 7	9	Q	S	S	S	15.7	S	S	2	2	S	S	4	4	4	4	4	14.5	4	4	4	4	4	4	4	4	14.3	4
	Score	177.5	168.5	167.5	162.5	162.5	162.5	161.5	160	158.5	158.5	157.5	156	154.5	152.5	152.5	150.5	150.5	150	149	149	149	149	148.5	148.5	147	147	146.5	146.5	146
	Result No.		7	ĸ	4	Ŋ	9	7	ω.	σ	10	11	12	13	14	15	16	17	18	19	20	77	22	23	24	25	56	27	28	53

RESULT 2 T49801

Fartmann, B.; Holland, R.; Nyakat

hypothetical protein B11B22.30 [imported] - Neurospora crassa C;Species: Dimi-2000 #sequence_revision 02-Jun-2000 #t;Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R;Reference number: Z5502 A;Recession: T49801 A;Reterence number: Z5502 A;Accession: T49801 A;Residues: preliminary A;Molecule Type: DNA A;Residues: 1-876 <SCH>A;Residues: 1-876 <SCH>A;Residues: BABL:AL356834; GSPDB:GN00116; NCSP:B11B22.30 A;Experimental source: BAC clone B11B22; strain OR74A

A; Map position: 6 A; Introns: 75/3; 190/1; 449/3

C;Genetics: A;Gene: NCSP:B11B22.30

chitinase (EC	hypothetical profe	TOUR 9 Prote	proling-rich proto	Protrie LLCI	promiserica	zyxın - chick	proline-rich	orobable pto	hymothotical	TROTICATOR	protein kinas	verprolin - v	T mothor C-H	DUTO II HOTEST Z II	recinota v re	RXR-betal isoform	proling-rich prote	TOTA SHAPPA	circumsporozoite p
821939	T27051	A86335	\$22373	196125	7777	A44300	T09024	F86387	T38236		5/6923	S51342	A34418	1727	101	184/18	S19560	900000	0.64QMB
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ALIGNMENTS

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hypothetical protein VSP-3 - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 14-011-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C;Accession: S50755
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Har
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 KTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPP 73
                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-473 <WOE>
A;Cross-references: EMBL:L29029; NID:g530875; PIDN:AAB53953.1; PID:g530876
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 473;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-574 <CON>
A;Cross-references: EMBL:298980; NID:e1060691; PIDN:CAB11718.1; GSPDB:GN00066; SPDB:6
A;Experimental source: strain 972h-; cosmid c4F10
C;Genetics:
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                                                                pombe)
                                        Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces pomter Species: Schizosaccharomyces pombe C; Date: 21-Jan-2000 *text_change 21-Jan-2000 (C; Date: 21-Jan-2000 *sequence_revision 21-Jan-2000 *text_change 21-Jan-2000 (C; Date: 21-Jan-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---IPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
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C;Date: 03-Dec1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 IQNISNNKTERSTA----PLNTQISA---LRNDPKPLPQQPPAPANQDQ----NSSQNT
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R; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, September 1997
A; Reference number: Z21813
A; Accession: T38819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 162.5; DB 2;
Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF038575; PIDN:AAB92587.1
A;Experimental source: strain JS21
C;Genetics:
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A; Introns: 72/3; 519/3; 564/1
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Best Local Similarity
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHE-associated splicing factor, long form - human

N/Alernate names: myoblast cell surface antigen 24.1D5; polypyrimidine tract-binding pr
C; Species: Homo sapiens (man)
C; Date: 21-26p-1093 #sequence_revision 18-Nov-1994 *text_change 24-Sep-1999
C; Date: 21-Sep-1993 #sequence_revision 0f SPF, a novel pre-mRNA splicing factor.
A; Reference number: A46302; MUD:93194059; PMID:8449401
A; Recession: A46302
A; Molecule type: mRNA
A; Residues: 1-707 cPAT>
A; Cross-references: EMBL:X70944; NID:93194059; PMID:8449401
A; Recession: A46302
A; Moste: sequence extracted from NCBI backbone (NCBIP:127206)
A; Recession: A4357; MUD:90091812; PMID:2480877
A; Cross-reference number: A4357; MUD:90091812; PMID:2480877
A; Reference number: A4357; MUD:90091812; PMID:2480877
A; Residues: 312-707 cOGW>
A; Cross-references: GB:X16850; NID:923711; PIDN:CAA34747.1; PID:923712
C; Genetics:
A; Map position: A4-49
C; Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein c; Superfamily: unassigned ribonucleoprotein repeat homology <RRMJ>
F; 372-438/Domain: ribonucleoprotein repeat homology <RRMJ>
F; 372-438/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                    10;
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                                                                                                                                                                                                      PTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVT 117
                                                                                                                                                                                                                                                                                                                                                                                                ----APAALTPAPP-----PPVTRKLT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 -PVSQGSNSSSADPKAPPPPVSSGEP-----PTLGENPDG----LSQE----- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 SPFSWLSRSSSKEQANPPPPPAAATAPRRNTASSVATLSSNPDGTLGKVDEEGNKNTLKD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGPKP-PIPPPPHQQQQPPPQQPPPHQQPPHQQQPPHQQQPPFPQQPSKPVV 111 CONTRACTOR CONTRACT
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                                                                                        Gaps
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            Length 876;
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    ; Score 168.5; DB 2;
; Pred. No. 0.012;
24; Mismatches 61;
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16.3%; Score 167.5; DB
Best Local Similarity 40.0%; Pred. No. 0.011;
Matches 54; Conservative 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFKQLRLREEGSAPTGDDDEKSSTPEEKE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---QLEHRER-SLQTLRDIQRMLFPDEKE 181
                                                                                                                                                                                                                                                                                                                                                                                            230 KSPPAAAAAAAAPPAP----
        16.4%;
30.1%;
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163 GAPPPTPPSSGVPTT 177
                                        L Similarity 30.1 63; Conservative
Query Match
Best Local S
Matches 63
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15.4%;
30.9%;
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Best Local Similarity 30,98
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.6 Best Local Similarity 31.3 Matches 52; Conservative
                                                                                                                                                                                                                                                                                            A; Gene: DR0458
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C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 24-Sep-1999
C:Accession: B56708
B:Zhou, G: Bao, Z.Q.; Dixon, J.E.
J. Biol. Chem. 270, 12665-12669, 1995
A:Title: Components of a new human protein kinase signal transduction pathway.
A:Recession: B56708
A:Return preliminary
A:Recession: B56708
A:Return preliminary
A:Residues: 1-815 < ZHO
A:Cross-references: GB:U25278; NID:g837260; PIDN:AA8B1381.1; PID:g837261
C:Superiamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo C:Reywords: ATP
F:52-315/Domain: protein kinase ATP-binding motif
              C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18535
C:Shimmada, K.; Harata, M.; Mizuno, S.
J. Call Sci. 110, 3031-3041, 1997
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick A;Reference number: Z18955; MuID:9803440; PMID:9365273
A;Ratus: preliminary; translated from GB/FMBL/DDBJ
A;Rotecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1151 <SHI>
A;Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 APAPKPAAPPRPLDRESPG------VENKLIPSVGSPASSTP-----LPPDGT 105
                                                                                                                                                                                                                                                                                                                                                                  33 PKPLPQQPPAPANQDQNSSQNTRLQPTP-PIPAPAPKPAAPPRP-----LDRESPGVE 84
                                                                                                                                                                                                                                                                                                                                                                                           17 RSTAPLNTQISALRNDPKPLP------QQPPAPANQDQNSSQNTRLQPTPPIP 63
  igh molecular mass nuclear antigen - chicken (fragment)
Species: Gallus gallus (chicken)
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPAAPALIISVPAPAPAPAPIPIPTPVQPISPPGPLAQPIGPQPQSAGSISGPVPQPACPPP
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                                                                                                                                                                                                                                                                                        Length 1151;
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                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 EPPTLGENPDGLSQEQ 157
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Best Local Similarity 33.1%
Matches 45; Conservative
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Best Local Similarity 32.19
Watches 54; Conservative
high molecular
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Gibecies: Delinococcus radiodurans (Strain KI)
Gispecies: Delinococcus radiodurans
Gismitch, Ho.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R..,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI.
A; Reference number: A75250; MUD: 20036896; PMID: 10567266
A; Status: preliminary
A; Mocession: F75518
A; Status: Preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule status: PRESCONSON (BB: ABENDO0513; NID: 96458129; PIDN: AAF10038.1; PID: 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyacession: S50754

R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Harr Plant Mol. Biol. 26, 947-960, 1994

A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <WOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
C;Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 PTPNAPACTPAPATCAPAACTPTACAPATCTPAPAACRPACCAPSPAPAPAACANAPA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 GSVVPEATVPESSTPAAPSAQTPPTPTRETAQTEASPAAPNSSAAPNEPASEPV-AGRP 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 *sequence_revision 21-Jul-1995 *text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 PKP-LPQQPPAPANQDQNSSQNTRLQP---TPPIPAPA---PKPAAP-PRPLDRESPGVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSPKASPSPSPKASPAPSPQPSPTPSPKASPVASPQOSPTPSPRPSPTPSPTP----SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:L29028; NID:9530877; PIDN:AAB53954.1; PID:9530878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 PTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PDTAASAGTPSAG
hypothetical protein - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 158.5; DB 2; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.6%; Score _ 0.055, 31.3%; Pred. No. 0.055, 4.75 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 VSQGSNSSSADPKAPP--PPPVSSGEPPT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPKASPPPSASPSASPSLSPKVSPSTPPT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 GTAASSPESASPVTVTPRGET---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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RESULT 10

RESULT

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characterization of a proline-rich gene expressed specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F4D11.90 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 04-Mar-2000 (Accession: T04455 (Species: N.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, April 1998 (A. Reference number: 215360 (A. Accession: T04455 (A. Mewes) (A. Residue: 1-731 (ABEV))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: F4D11.90
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T05441
R; Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schue submitted to the Protein Sequence Database, November 1998
A; Reference number: 215416
A; Accession: T05441
                                                                                                                                                                                                                     ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRPLDRESPGVENKLIPSVGSPASSTPL-----PPDGTGPNST-PNNRAVTPVSQG- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                       62 PSPKPGPSPSPRPPSPARPVP-----PPSPSPKPSPPKPPAPSPKP-SPPKPP 111
                                                                                                                                                                                                                                                                                                                                                    93 ----SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                 2 PKPQPKPPPKPQPKPPPAPTPSPCPPQPKPQPKPPAPTPSPCPPQPPKPQPKPPAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPK--PAAP
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 -----SNSSSADPKAPP------PPPVSSGEPPTLGENPDGLSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 731,
                                                                                                                                                               Score 156; DB 2; Length 44
Pred. No. 0.03;
9; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proline-rich protein F7K2.50 - Arabidopsis thaliana (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 326/1; 476/1; 505/1; 528/3; 557/2; 606/3; 660/3
A;Note: F4D11.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone F4D11 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-379 <BEV>
A;Cross-references: EMBL:AL033545
A;Experimental source: cultivar Columbia; BAC clone F7K2
                                                                                                           A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%; Score 154.5; DE ilarity 27.6%; Pred. No. 0.06; Conservative 20; Mismatches
                                                                                                                                                            Query Match
Best Local Similarity 33.3%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: AL022537
A; Description: Cloning and A; Reference number: $16748
                                         A, Accession: S16748
A, Molecule type: mRNA
A; Residues: 1-449 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches
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S16748
Stoches
Proline-rich protein - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S16748
B;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. submitted to the EMBL Data Library, August 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extensin - Volvox carteri (fragment)
C;Species: Volvox carteri
C;Species: Volvox carteri
C;Date: 04-Dec-1992 #text_change 21-Jul-2000
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000
C;Accession: S22697; S21006
R;Ertl, H.; Hallmann, A.; Wenzl, S.; Sumper, M.
BMBO J. 10, 2055-2062, 1992
A;Title: A novel extensin that may organize extracellular matrix biogenesis in Volvox of Reference number: S22697; MUID:92289669; PMID:1600938
A;Accession: S22697
A;Residues: 1-464 <HAL>
A;Residues: 1-464 <HAL>
A;Cross-references: EMBL:X65165; NID:921991; PIDN:CAA46283.1; PID:921992
C;Keywords: 91ycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P----AAPPRPLDRESPGVENKLIPSVGSPASSTPLP---PDGTGPNSTPNNRAVTPV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPP-PPVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 KTERSTAPLNTQISALRNDPKPLP--QQPPAPANQDQNSSQNTRLQP---TPPIPAPAPK 68
                             C:Species: Zea mays (maize)
C:Species: Zea mays (maize)
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C:Accession: 84915
A:Description: Pex genes pollen-specific genes with extensin-like domains. A:Description: Pex genes pollen-specific genes with extensin-like domains. A:Decession: 84915
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-1188 <RUB>A:Cross-references: EMBL:234465; NID:g600117; PIDN:CAA84230.1; PID:g600118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 PLNTQISALRNDPKPLPQQPPAPANGDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRES
                                                                                                                                                                                                                                                                                                                                                                                              19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                  Length 1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                       15.4%; Score 158.5; DB 2; 32.0%; Pred. No. 0.057; Wiematches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1078 PPAPVSSPPPVKSPPPPAPVSSPPPPIKSPPP 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGSNSSSADP-KAPPPP-PVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 32.09
49; Conservative
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            extensin-like protein - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 SGEPPTLGENP 150
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                   Best_Local
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extensin-like protein [imported] - Arabidopsis thaliana .

C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Dereb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C.Accession: D85257
B.Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Mature 402, 769-777, 1999
A.Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A.Reference number: A85001; MUID:20083488; PMID:10617198
A.Accession: D85257
A.Acc
                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 SVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTLGEN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 SVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGEN 149
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                                                                                                                                                                                                                                                                                                                                                                        33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPI---PAPAPKPAAPPRPLDRESPGVENKLIP 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Gaps
                                                                                                                               Ouery Match
14.8%; Score 152.5; DB 2; Length 379;
Best Local Similarity 31.8%; Pred. No. 0.041;
Matches 41; Conservative 12; Mismatches 45; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 379;
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14.8%; Score 152.5; DB 2; Length:
Best Local Similarity 31.8%; Pred. No. 0.041;
Matches 41; Conservative 12; Mismatches 45; Indels
A;Note: F7K2.50
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 15, 2003, 10:33:12 Job time : 48.0467 secs
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D85257
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 15, 2003, 10:27:32; Search time 23.4008 Seconds (without alignments) 389.867 Million cell updates/sec Run on:

US-09-915-543-15_COPY_199_392

1 TIVSFHIQNISNNKTERSTA..........LFDDEKEFTGAQSGGPQQNP 194 Perfect score: Sednence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	000512 homo sapien	homo	homod	Q9fpq6 chlamydomon	_	brass	homo	homo	P28702 homo sapien	homo	nicot		_		plasmod	Q04584 gallus gall		Sacc	mus	รกพ	Q05859 mus musculu	-					Pome 8		medi		_	rattu	Q9y566 homo sapien
(I	BCL9_HUMAN	SFPQ_HUMAN	MK07_HUMAN	GP1_CHLRE	ENAH_MOUSE	APG_BRANA	WAIP_HUMAN	PRP2_HUMAN	RXRB_HUMAN	MUC2_HUMAN	EXLP_TOBAC	CSP_PLABA	APG_ARATH	SHK1_RAT	CSP_PLABE	ZYX_CHICK	SPKC_SYNY3	VRP1_YEAST	RXRB_MOUSE	PRP3_MOUSE	FM14_MOUSE	FMN1_MOUSE	PRPL_HUMAN	EXTN_SORBI	WASL_HUMAN	EXTN_TOBAC	MNT_HUMAN	MK07_MOUSE	NO20_MEDTR	WASL_BOVIN	SLP1_CLOTM	WASL_RAT	SHK1_HUMAN
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Length	1426	707	815	555	802	449	503	251	533	5179	426	347	534	2167	339	542	535	817	520	296	1206	1468	276	283	505	620	582	806	268	505	1664	501	2161
% Query Match	9.66	•	'n	15.5	'n	5	4.	14.6	4	4.	4.	4	14.2	4	4	4	14.0	14.0	14.0	æ.		ä.									13.6	•	13.5
Score	1024	167.5	161.5	159.5	158	156	151.5	150.5	150.5	150	149	147	146	146	144.5	144.5	4	4		143	4	4						4	•	œ,	39	13	138.5
Result No.	-	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

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	P05142 mus musculu O10341 orqyia pseu							
TEGU_HSV11 PRPM_HUMAN	PRP2_MOUSE Y091_NPVOP	GAG_SMSAV	RXRB_RAT	DIA1_HUMAN	AEX3_CAEEL	BAT2_HUMAN	LA17_YEAST	SYNIMOUSE
т,			1 ~	П	щ	Н	Н	Н
3164 234	261 279	512	458	1248	1409	2142	633	670
13.5	13,3 13,3	13.3	13.3	13.3	13.3	13.3	13.2	13.2
138.5	137	137	136.5	136.5	136.5	136.5	136	136
3.5 3.5	36	886	40	41	42	43	44	45

ALIGNMENTS

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colon and blood.
--- DISEASE involved in a t(1;14)(q21;q32) chromosomal translocation found in a patient with precusor B-cell acute lymphoblastic leukemia (ALL). This translocation leaves the coding region intact, but may have pathogenic effects due to alterations in the expression level of BCL9. Several cases of translocations within the 3' untranslated region of BCL9 have been found in B-cell
                                                                                                                                                                               MEDLINE=98158621; PubMed=9490669; Willis T.G., Zalcberg I.R., Coignet L.J.A., Wlodarska I., Stul M., Jadayel D.M., Bastard C., Treleaven J.G., Catovsky D., Silva M.L.M.,
                                                                                                                                                                                                                            "Molecular cloning of translocation t(1;14)(q21;q32) defines a novel
                                                                                             Bomo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                          28-FEB-2003 (Rel. 41, Created)
B-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
B-cell lymphoma 9 protein (Bcl-9) (Legless homolog).
                    PRT; 1426 AA.
                                                                                                                                                                                                                                        gene (BCL9) at chromosome 1q21.";
Blood 91:1873-1881(1998).
                       STANDARD;
                                                                                                                                                                       brain;
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                       rissum-retal
                       BCL9_HUMAN
                                                                                                                                                                                                                                                                             FUNCTION.
                                000512;
          BCL9_HUMAN
RESULT 1
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61 PIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVS 120
                                                                                                                                                                                                                                                                 1 TIVSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fetal skeletal muscle;
MEDLINE-90091812; PubMed-2480877;
Gower H.J., Moore S.E., Dickson G., Elsom V.L., Nayak R., Walsh F.S.;
"Cloning and characterization of a myoblast cell surface antigen defined by 24.1D5 monoclonal antibody.";
Development 105:723-731(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 48-68 AND 213-246.
MEDLINE-93176127; DUDMed-8439294;
Shang W.-W., Zhang L.-X., Busch R.K., Farres J., Busch H.;
"Purification and characterization of a DNA-binding heterodimer of 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p23246; p30808;
01-007-1991 (Rel. 20, Created)
01-007-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Splicing factor, profilme-and glutamine-rich (Pplypyrimidine tract-
binding protein-associated splicing factor) (FPB-associated splicing
factor) (FSF) (DNA-binding P52/P100 complex, 100 kDa subunit).
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patton J.G., Porro E.B., Galceran J., Tempst P., Nadal-Ginard B., *Cloning and characterization of PSF, a novel pre-mRNA splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                       Score 1024; DB 1; Length 1426; Pred. No. 4.3e-45;
                                                           Nuclear protein; Chromosomal translocation; Proto-oncogene;
                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                             970 973 POLY-PRO 3.
1426 AA; 149314 MW; A240A487716B7F1B CRC64;
                                                                                                   CINNB1-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707 A.A.
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                   POLY-PRO 1. POLY-PRO 2.
                                                                                                                                                 POLY-ALA.
                                                                                       PRO-RICH.
EMBL; Y13620; CAA73942.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                           GO; GO:0007048; P:oncogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93194059; PubMed=8449401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 100 kDa from HeLa cells.";
Biochem. J. 290:267-272(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 312-707 FROM N.A.
                                                                                                                                                                                                         99.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EFTGAOSGGPOONP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes Dev. 7:393-406(1993).
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
          Genew, HGNC:1008; BCL9.
MIM; 602597; -.
                                                                                                                  335
517
903
973
                                                                       Wnt signaling pathway.
DOMAIN 231 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFPO OR PSF.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Fetal brain;
                                                                                                                                                                                                                 al Similarity
193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFPQ_HUMAN
                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 RNDPKPLPQQPPAPANQDQN--SSQNTRLQPTPPIPAPAPKP----AAPPRPLDRESPGV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTERFGQGGAGPVGGQGPRGMGPGTPAGYGRGREEYEGPNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Indels 29; Gaps
FUNCTION: ESSENTIAL PRE-MRNA SPLICING FACTOR REQUIRED EARLY IN SPLICEDOSOME FORMATION. BINDS TO THE MAMMALIAN POLYPYRIMIDINE TRACTS. FORMS A COMPLEX WITH THE POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTS). SEEMS TO ALSO BIND DNA. STORY THE PROTEIN (PTS). SEEMS TO ALSO BIND DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM; RNP_1; 1.
Nuclear protein; RNA-binding; DNA-binding; mRNA splicing; Repeat;
Alternative splicing; RNA-BINDING (RRM) 1.
                                                                                                                                                                              INSOIG-P23246-2; Sequence-VSP_005855; SIMILARITY: Contains 2 RNA recognition motif (RRM) domains. CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE MYOBLAST CELL CRUTHON: WAS ORIGINALLY (REF. 2) THOUGHT TO BE MYOBLAST CELL SURREACE ANTICEN A4. 1D5 AND A POSSIBLE MEMBRARE-BOUND PROPEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPRF -> VRMIDVG (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.3%; Score 167.5; DB 1; Length 707; Best Local Similarity 40.0%; Pred. No. 0.031; Aatches 54; Conservative 5; Mismatches 47; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO: GO:0008248; F:pre-mRNA splicing factor activity; TAS. GO: GO:0006371; P:mRNA splicing; TAS. InterPro: IPR000564; RNA_rec_mot. Pfam; PF00076; rrm; 2. SWART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
3 x 3 AA REPEATS OF R-G-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G -> R (IN REF. 3).
6D8D5EA95E235847 CRC64;
                                                                                                      Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLN/GLU/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP 005855
                                                                                                                                                   IsoId=P23246-1; Sequence=Displayed;
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POLY-GLN.
POLY-PRO.
POLY-PRO.
POLY-PRO.
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POLY-GLY.
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                                                                         -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           707 AA; 76149 MW;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X70944; CAA50283.1; -. EMBL; X16850; CAA34747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A46302, A46302.
HSSP; P11940; ICVJ.
SWISS-2DPAGE; P23246; HUMAN.
Genew; HGNC:10774; SFPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECTOKINASE.
                                                                                                                                                                    Name=Short;
                                                                                                                                       Name=Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 605199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GK; P23246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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DOMAIN
REPEAT
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                                   ---PDGTGPNSTPN-NRAVTPVSQGSNSSSADP 130
                                                                                                                                                                                                                                                                                                                                  MKO7_HUMAN STANDARD; PRT; 815 AA.
013164; 016634;
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-4001 (Rel. 40, Last annotation update)
16-OCT-5001 (Rel. 5) (ERK-5) (ERK-5) (ERK-5) (ERK-5) (ERK-5) (ERK-5) (ERK-6) (ERK-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee J.-D., Ulevitch R.J., Han J.;
"Primary structure of BMK1: a new mammalian map kinase.";
Biochem Biophys. Res. Commun. 213:715-724(1995).
-!- FUNCTION: MEKS AND ERKS INTERACT SPECIFICALLY WITH ONE ANOTHER AND
NOT WITH MEKL/FRKI OR MEKZ/ERK2 PATHWAYS.
-!- ENZYME REGULATION: Activated by tyrosine and threonine
phosphorylathon (By similarity).
-!- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES. ABUNDANT IN
HEART, PLACENTA, DUNG, KIDNEY AND SKELETAL MUSCLE. NOT DETECTABLE
IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou G., Bao Z.Q., Dixon J.E.; "Components of a new human protein kinase signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 602521; -.
GO; 600:004707; F:MAP Kinase activity; TAS.
GO; 60:0007165; P:signal transduction; TAS.
InterPro; IPR003527; MAP_Kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 270:12665-12669(1995).
   EN--KLIPSVGS--PASSTPLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fetal brain;
MEDLINE-95279403; Pubmed=7759517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95374539; PubMed=7646528;
                                                                                                                          131 KAPPPPPVSSGEPPT 145
                                                                                                                                                                 163 GAPPTTPSSGVPTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U29725; AAA81381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U29726; AAA82932.1; -.
EMBL; U29727; AAA82933.1; -.
PIR; B56708; B56708.
HSSP; P24941; IHCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:6880; MAPK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROLE, IS ABSENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60252
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576 RPAAPALTSVPAPAPAPTPTPTPVQPTSPPGPLAQPTGPQPQSAGSTSGPVPQPACPPP 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 APARPAAPPRPLDRESPG----VENKLIPSVGSPASSTP----LPPDGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              636 GPAPHPTGPPGPIPVPAPPQIATSTSLLAAQSLVPPPGLPGSSTPGVLPYFPPGLPPPDA 695
                                                  SMART; SM00220; S_TKC; 1.
PROSITE; PS01351; MARK; 1.
PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_OM; 1.
PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                         ----QOPPAPANODQNSSQNTRLQPTPPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Glycosylated polyproline II rods-with-kinks as a structural motif in
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
(BY SIMILARITY).
(BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE)
PHOSPHORYLATION (ACTIVATES THE KINASE)
                                                                                                                                                                                                                                                                                                     AREGRIRPHRCLCS -> GPVKVEPAHTAASVA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-21159092; PubMed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91017504; PubMed-1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                  Score 161.5; DB 1; Length 815;
Pred. No. 0.069;
7; Mismatches 64; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G--PNS----TPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> V (IN REF. 2).
379AD69803207CCF CRC64;
                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                               (IN REF.
                                                                                                                                                PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555 AA
                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxyproline-rich glycoproteins.";
                                                                                                                                                           POLY-ALA.
PRO-RICH 1.
                                                                                                                                                                                   POLY-ARG.
PRO-RICH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL PRELIMINARY SEQUENCE FROM N.A.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                        Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant hydroxyproline-rich glycopi
Biochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                     17 RSTAPLNTQISALRNDPKPLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                            88636 MW;
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32.1%;
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346
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340
5523
699
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181
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MOD_RES
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                                                                                                                                                                                                             NP_BIND
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GP1_CHLRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97015079; PubMed-8861907;
Gertler F.B., Niebuhr K., Reinhard M., Wehland J., Soriano P.;
"Mena, a relative of VASP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4 AND 5), FUNCTION, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENAH_MOUSE STANDARD; PRT; 802 AA.

403177; $70431; $70431; $70433;

01-CCT-1996 (Rel. 34, Created)

15-SEP-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Enabled protein homolog (NPC derived proline-rich protein 1) (NDPP-1).

ENAH OR MENA OR NDPP.
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIP----APAPKPAAPPRPLDRESPGVENKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 PSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sazuka T., Tomooka Y., Kathju S., Ikawa Y., Noda M., Kumar S.; "Identification of a developmentally regulated gene in the mouse central nervous system which encodes a novel proline rich protein."; Blochim. Blophys. Acta 1132:240-248(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                              VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 159.5; DB Pred. No. 0.063;
                                              -1- SUBUNIT: Associates with GP2 and GP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
                                                                                                                                                                                                                                         EMBL; M58496; AAA69706.1; ALT_SEQ. GlycosuiteDB; Q9FPQ6; InterPro; IPR002965; Prich_extensn. InterPro; IPR003883; Pistil_extensin. PRINTS; PR01217; PRICHEXTENSN. PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93041923; PubMed=1420303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54219 MW;
                                                                                                                                                                                                                                                                                                                                                Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.5%;
                                                                                                                                                                                                                            EMBL; AF309494; AAG45420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 32.8 tes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                           555
339
279
455
493
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399
455
455
555 AA;
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                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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ENAH_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNRPLTGLAAAIAGA -> HRALSWDHLHLRHHPLSHQALP
TPQHFLLPQDPLHHLHCHPLVLLIHPLHHPLFLIKLLPLLP
                                  MEDINE-99166867; PubMed-10069337;
Lanier L.M., Gates M.A., Witke W., Menzies A.S., Wehman A.M.,
Macklis J.D., Kwiatkowski D., Soriano P., Gertler F.B.;
Man is required for neurulation and commissure formation.";
Neuron 22:313-325(1999).

1- FUNCTION: May be involved in microfilament assembly and cell
motility. Induces the formation of F-actin rich outgrowths in
fibroblasts. Required for neurulation and commissure formation.

1- SUBGINIT: Binds profilin.

1- SUBCELIULAR LOCATION: Localized to focal adhesions and, to a
                                                                                                                                                                                                                                                                                                                                             Name-4: Synonyms-Mena+:
IsoId=Q03173-5: Sequence-VSP_007257, VSP_007258;
TISSUE SPECIFICITY: IN THE HEART AND TESTIS AND LESS SO IN THE
LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS AND BRAIN.
SIMILARITY: Contains 1 WH1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLLPLPSPHLEFSLDPROKTIAFNWTCSCNCGS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wissing (in isoform 2 and isoform 3). /FrId=VSP_007259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurogenesis; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 4).
/FTId=VSP_007257.
CIFC -> VFYL (in isoform 4).
/FTId=VSP_007258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 2).
/FTId=VSP_007260.
592BB975EE20F77F CRC64;
                                                                                                                                                                                                                                                                          IsoId=Q03173-2; Sequence=VSP_007255, VSP_007256;
Name=2; Synonyms=Mena;
                                                                                                                                                                                                                                                                                                     IsoId=Q03173-3; Sequence=VSP_007259, VSP_007260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 1).
                                                                                                                                                                                        lesser extent, leading edges and stress fibers
                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTId=VSP_007256
                                                                                                                                                                                                                                                                                                                    Name=3; Synonyms=Mena+;
IsoId=003173-4; Sequence=VSP_007259;
                                                                                                                                                                                                                               Name=5; Synonyms-Mena+++;
ISoId=Q03173-1; Sequence=Displayed;
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POLY-PRO.
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D10727; BAA01570.1; --
EMBL; U72520; AAC52863.1; --
EMBL; U72521; AAC52864.1; --
EMBL; U72522; AAC52865.1; --
EMBL; U72523; AAC52866.1; --
EMBL; U72523; AAC52866.1; --
PIR; S27200; S27200.
INTERPRO; EPRO01960; WH1.
Pfam; PF00568; WH1; 1.
SWART; SMO0461; WH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85844 MW;
                                                                                                                                                                                                    -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135
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                            SUBUNIT
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DOMAIN 1
DOMAIN 442
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                                        10;
                                                                                                      NKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPPGKATGPRPVLPVCVS 407
                                                                                                                                                                            408 SPVPQMPPSPTAPNGSLDSVTYPVSPPPTSGPAAPPPPPPPPPPPPPPPPPPPPPLPPLAS 467
                                                                                                                                                                                                               ----DRESPGVENKLI-------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV- 116
                                                                                                                                                                                                                                               468 LSHCGSQASPPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGDSSASEPGLQAAS 527
                                                                                                                                              92
                                                                           ----- 33
                                                                                                                                             -SSQNTRLQPTPPIPAPAPKPAAPPRPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Draper J., Scott R.;
"Gametophytic and sporophytic expression of an anther-specific
"Gametophytic and sporophytic expression of an anther-specific
Arabidopsis thallana gene.";
Plant J. 3:111.120(1993).
-!- TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGRESIS, DURING
MICROSPORE DEVELOPMENT, HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94004980; Pubmed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anter-specific proline-rich protein APG (Protein CEX) (Fragment)
                                        88;
     DB 1; Length 802;
                                                                                                                                                                                                                                                                                    ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                     OPAESPIPOG--LVLGPPAPPPPPLPSGPAYASALPPPGPPP 569
                                        Indels
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                                      62;
                                                                         ----OISALRNDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 32, Last annotation update)
                    0.1;
                                                                                                                                                                                                                                                                                                                                                                                                               449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY. POTENTIAL.
                     Pred. No. 0.1; ; Mismatches
     15.4%; Score 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01098; LIPASE_GDSL_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001087; Lipase_GDSL.
                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48779 MW;
                                                                     13 NKTERSTAPLNT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00657; Lipase_GDSL; 1. PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X60376; CAA42924.1; -.
                    26.3%;
                                                                                                                                         34 KPLPQQPPAPANQDQN-
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APG OR ČEX.
Brassica napus (Rape).
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Query Match
Best Local Similarity
Matches 59; Conserv
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01-NOV-1995
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ACT_SITE
SEQUENCE
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Length 449;

DB 1;

No. 0.079;

Score 156; Pred. No. 0

15.2%; 33.3%;

Query Match Best Local Similarity

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                                33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVG 92
                                                                              61
                                                                                                                                               62 PSPKPGPSPSPPKPPPSPAPKPVP-----PPSPSPKPSPKPPAPSPKP-SPPKPP 111
                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Wiskott-Addrich syndrome protein interacting protein (WASP interacting
                                                                  2 РКРОРКРЕРКРОРКРОРКРОТРЯРСРРОВРЕТОРКОРКРОРКРОРАРТЬ
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells.";
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GO; GO:0015629; C:actin cytoskeleton; TAS.
GO; GO:0003779; F:actin binding activity; TAS.
GO; GO:0003552; F:profilin binding activity; TAS.
GO; GO:0008154; P:actin polymerization and/or depolymerization; TAS.
GO; GO:000661; P:protein complex assembly; TAS.
InterPro: IPR003124; WH2.
                                                                                                         93 ----SPASSIPLPPDGIGPNSIPNNRAVIPVSQGSNSSSADPKAPPPPVSSGEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interacting protein.";
J. Immunol. 162:5019-5024(1999).
J. Immunol. 162:5019-5024(1999).
I. Timmunol. 162:5019-5024(1999).
I. FUNCTION: MAY HAVE DIRECT ACTIVITY ON THE ACTIN CYTOSKELETON.
INDUCES ACTIN POLYMERIZATION AND REDISFRIBUTION.
I. SUBBUIT: BINDS TO WASP, PROFILIN AND ACTIN.
I. SUBBUIT: BINDS TO WASP, PROFILIN AND ACTIN.
ITSUE SPECIFICITY: HIGHLY EXPRESSED IN PERIPHERAL BLOOD MONONUCLEAR CELLS, SPLEEN, PLACENTR, SMALL INTESTIN, COLON, THYMUS. LOWER EXPRESSION IN OVARY, HEART, BRAIN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98070810; PubMed-9405671;
MEDLINE-98070810; NubMed-9405671;
MEMP, a protein associated with Wiskott-Aldrich syndrome protein, induces actin polymerization and redistribution in lymphoid cells.

Proc. Natl. Acad. Sci. U.S.A. 94:14671-14676(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interaction of Wiskott-Aldrich syndrome protein (WASP) with WASP
    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           impair the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kreideweiss S., Delany-Heiken P., Nordheim A., Ruhlmann
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart D.M., Tian L., Nelson D.L.; *Mutations that cause the Wiskott-Aldrich syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND VARIANT ALA-495
  57;
                                                                                                                                                                                                                                                      503 AA.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 192-503 FROM N.A., ANI
MEDLINE=99218549; PubMed=10202051;
9
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16-001-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last anno
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EMBL; AF106062; AAD45972.1; -.
EMBL; X86019; CAA60014.1; -.
                                                                                                                                                                                                                                                                                                                                                                   protein) (PRPL-2 protein).
WASPIP OR WIP.
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39; Conservative
                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                 protein)
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                 60 PPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAV--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                           346 PPLPSPGRSGPLPPPPSERPPPPVRD-----PPGRSGPLPPPPPPVSRNGSTSRALPAT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 POLPSRSGVDSPRSGPRPPLPPDRPSAGAPPPPPPSTSIRNGFQDSP---CEDEWESRFY 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 --TPVSQGSNSSSADPK-----APPPPPPVSSGEPPTLGENPDGLSQEQLEHR-- 161
                                                                                                                                                                                                                                                                                                                                            12 NNK----TERSTAPLNTQISALRNDFKPLPQQPPAPANQDQNS-----SQNTRL-QPT 59
                                                                                                                                                                                             PHRPHLR -> SSQAPPP (IN REF. 3).
P -> PV (IN REF. 2).
GSNRRERGGPPLPPIPR -> EYFCQGF (IN REF. 2).
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary proline-rich protein precursor (Clone CP7) [Contains: Basic peptide P-F] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saitch E., Isemura S., Sanada K.;
Complete amino acid sequence of a basic proline-rich peptide, P-F,
from human parchid saliva.";
J. Biochem. 93:883-888(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maeda N., Kim H.-S., Azen E.A., Smithies O., "Differential RNA splicing and post-translational cleavages in the human salivary proline-rich protein gene system."; J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                             14.7%; Score 151.5; DB 1; Length 503; 26.5%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 FHPISDLPPPEPYVQTTKSYPSKLARNESR-SGSNRRERGGPPLPP 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 -----ERSLQTLRDIQRMLFPDEKEFTGA---QSGGPQQNP 194
                                                                                                                                                                                                                                                                                                            84; Indels
                                                                                                                                                                                                                                             43EB88674DD3BF1A CRC64;
                                                                                              XRSGPXPPXP MOTIF 1. XRSGPXPPXP MOTIF 2. XRSGPXPPXP MOTIF 3.
                                                                                                                                                                               /FTId=VAR_010295.
                                                                                                                                               ACTIN BINDING.
                                                                                                                                                                                                                                                                                                             25; Mismatches
                                                  GLY-RICH.
POLY-SER.
                                    POLY-PRO.
                                                                                 PRO-RICH
SMART; SM00246; WH2; 1.
Actin-binding; Repeat; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 134-194.
MEDLINE=83265674; PubMed=6874669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                               51489 MW;
                                                                                                                                                                                                                                                                                                             60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                              361
                                                                                                                                             48
                                                                                                                                                                                               309
                                                                                                                                                                                                                              487
503 AA;
                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 IDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 NDPK--PLPQQPPAPANQDQNSSQNTRLQPTPP------IPAPAPKPAAPRP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification, cloning, and RXR identity of the HeLa cell factor with which RAR or TR heterodimerizes to bind target sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92253386; PubMed=1315958;
Fleischhauer K., Park J.H., Disanto J.P., Marks M.S., Ozato K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation of a full-length cDNA clone encoding a N-terminally variant form of the human retinoid X receptor beta."; Nucleic Acids Res. 20:1801-1801(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Breast carcinoma;
MEDLINE-92127595; PubMed-1310259;
Leid M., Kastner P., Lyons R., Nakshatri H., Saunders M.,
Zacharewsi T., Chen J.Y., Staub A., Garnler J.M., Mader S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leid M., Kastner P., Lyons R., Nakshatri H., Saunders M.,
Zacharewsi T., Chen J.Y., Staub A., Garnier J.M., Mader S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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71
133
195
24641 MW; D779F590COEBF30B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%; Score 150.5; DB 1;
31.2%; Pred. No. 0.091;
tive 9; Mismatches 61;
                                                                                                                                                                                                                      BASIC PEPTIDE P-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FXRE_HUMAN STANDARD; PRT; 533 AA. P28702; P28703; 01-D802-1992 (Rel. 24, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                                                                                                                                                              Repeat; Parotid gland; Multigene family.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93046692; PubMed=1330328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 PP-VSSGEPPTLGENPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 PPGKPQGPPPQGGNKPQG 173
                             EMBL; K03208; AAA60189.1; -. PIR; E25372; PIHUPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Conservative
                                                           194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 68:377-395(1992).
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                                                                                                                                                                                                                                                                                                                                                                  251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                           A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Idschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.", Male Proc. Mall. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-Short;
Isoid-PERF02-2; Sequence-Not described;
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
                                                                                              Corella A., Vergara A., Paez G., de Miguel C., Encio I.; *Molecular cloning and characterization of the human HRXRB gene and 5'
Numasawa T., Koga H., Ueyama K., Maeda S., Sakou T., Harata S., Leppert M., Inoue I.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0004886; F:retinoid-X receptor activity; TAS. GO:0003713; F:transcription co-activator activity; TAS.
                                                                                                                                                         Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P28702-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Nuclear.
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TRANSFAC; T01334; -.
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                                                                                                                                          flanking region
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                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                            31 NDPKPLPQ--QPPAPANQDQNSSQNTRLQPTPPIPAPA------PKPAAPPRPLDRESP
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                                                                                                                                                                                                                                                                                                                                                               14.6%; Score 150.5; DB 1; Length 533;
31.0%; Pred. No. 0.17;
tive 11; Mismatches 45; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.; "Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor.";
J. Biol. Chem. 269:2440-2446(1994).
                                                                                                 Print.,
Probom; PD000035; ...__
SMART; SM00390; ZnF_C4; 1.
SMART; SM00399; ZnF_C4; 1.
SMOSTE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing; 3D-structure.

MODGLARR RECEPTOR-TYPE.

.770 NUCLEAR RECEPTOR-TYPE.
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Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            both upstream and downstream of its central repetitive region.";
J. Biol. Chem. 267:21375-21383(1992).
[3]
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D0069FE93AC16A04 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.
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InterPro; IPR000536; Hormone_rec_lig. InterPro; IPR001723; Stdhrmn_receptor.
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C4-TYPE.
HINGE.
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                                                                        PRINTS, PRO0398; STRDHORMONER.
PRINTS, PRO0047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
                                 InterPro; IPR001628; Znf_C4steroid.
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MEDLINE-94132002; PubMed-8300571;
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                                           Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-c4; 1.
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EXLP_TOBAC
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                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 AGENTS AT MUCOSAL SURFACES.

-1 SUBUNIT: MULTIMERIC.
-1 SUBUNIT: MULTIMERIC.
-1 SUBUNIT: MULTIMERIC.
-1 SUBUNIT: MULTIMERIC.
-1 SUBCELLULAR LOCATION: Secreted.
-1 TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS, BRONCHUS, CERVIX AND GALL BLADDER.
-1 PTH. ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
-1 POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLEIES.
-1 SIMILARITY: CONTAINS 1 C-terminal cystine knot-like (CTCK) domain.
-1 SIMILARITY: Contains 1 TLL (Trypsin inhibitory-like) domain.
                                     "MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorphism.";
J. Clin. Invest. 88:1005-1013(1991).
J. Clin. Invest. 88:1005-1013(1991).
J. Clin. Invest. 88:1005-1013(1991).
J. Clin. Invest. BRIDGATING OFFICE INTESTINES, AIRMAYS, AND OTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A PROTECTIVE, LUBRICATING BARRIER AGAINST PARTICLES AND INFECTIOUS
MEDLINE-91358717; PubMed-1885763;
Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W.,
Petersen G.M., Klm Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUCIN 2.
APPROXIMATE REPEATS
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GO; GO:0005803; C:secretory vesicle; TAS.
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PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00225; EGF_1; UNKNOWN_1.
PROSITE; PS01208; VWFC_1; 2.
PROSITE; PS50184; VWFC_2; 2.
Glycoprotein; Repeat; Signal.
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InterPro; IPR006208; Cys_knot_C.
InterPro; IPR006209; EGF_like.
InterPro; IPR001007; VWF_C.
InterPro; IPR001096; VWF_D.
Pfam; PF00007; Cys_knot; I.
Pfam; PF00093; Vwc; I.
Pfam; PF00094; Vwc; I.
Pfam; PF00094; Vwc; I.
SMART; SM00216; VWC; Z.
SMART; SM00216; VWD; 4.
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EMBL; M74027; AAA59875.1; --
EMBL; M94131; AAA59163.1; --
EMBL; M9432; AAA59164.1; --
PIR; A49963; A43932.
Genew; HGNC:7512; MUC2.
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1487 PTTTTTTPPPTTTPSPPMTTPITP----PASTTTLPPTTTPSPPTTTTTPPPTTTTPPSPPTTTFS
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T -> S (IN REF. 3).
L -> P (IN REF. 3).
M -> T (IN REF. 3).
G -> S (IN REF. 2).
MW, BSCD7571FB9A5663 CRC64;
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BY SIMILARITY.
N-LINKED GLCNAC.
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540295 MW; 8
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APG_ARATH
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                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 PSVGSPASSTPLPPDGT-GPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVS----- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 NDPKPLPQQPPAPANQDQNS--SQNTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                            PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Peprmatophyta; Paprmatophyta; Paprmatophyta; Ragnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
51A495CC94017812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 SSPSPLVKPPPPPPPSPCKPSPDQSAKQPPQPP-PAKQPSPPPPPPVKAPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-11ke protein precursor (PELP).
Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                       Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%; Score 149; DB 1
29.9%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                           STRAIN=cv. Petit Havana; TISSUE=Pistil;
MEDLINE=93005740; PubMed=1392607;
                                                                                                                                                                                                                                                                                                                                   PIR; JQ1696; JQ1696.
Interpro; IPR006041; Ole_el_ext.
Interpro; IPR002965; P_rich_extensn.
Interpro; IPR003882; Pistil_extensln.
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01190; PO116n_01e_e_I; 1.
PRINTS; PR01217; PRICHEXTERSN.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44278 MW;
                                                                                                                                                                                                                                                                                                                        EMBL; Z14019; CAA78397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSPAAEPPIIAPFP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               73
80
87
182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
310
426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 40; Conserv
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                        POLLINATION
                                                                                                                                                                                                                                                                                                                                  JQ1696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSP_PLABA
ID CSP_P
AC P2309
DT 01-NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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¥

347

PRT;

STANDARD;

CSP_PLABA P23093;

01-NOV-1991 (Rel. 20, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 APAPKPAAPPRPLDRESPGVENKLIPSVGSPA---SSTPLPPDGTGP----NSTPNNRA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 PPNPNDPPPPNPNDPPPNANDPPPNANDPAPPNANDPAPPNANDPAPPNANDPAPPNANDPPPNAN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ONISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPP----IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SUBFACE ANTIGEN OF THE ORGANISM.
-1- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                          protein gene from the ANKA clone 2.34L.";
Nucleic Acids Res. 18:376-376(1990).
-!- FUNCTION: THE CIRCUMSPORZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPORZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                           MEDLINE-90221834; PubMed-2183186;
Lockyer M.J., Davies C.S., Suhrbier A., Sinden R.E.;
"Nucleotide sequence of the Plasmodium berghei circumsporozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 X 8 AA REPEATS.
17 X 2 AA REPEATS OF P-Q.
TSP TYPE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OEC240EE35681AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
APG OR ATIG20130 OR 120H2.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 VTPVSQGSNSSSADPKA--PPPPPVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 NDPPPPNPN-DPAPPNANDPPPPNPNPAPPOGNNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APC_ARATH STANCE,
APC_ARATH STANCE,
P40602; Q93214; Q9LNT8;
01-FEB-1995 (Rel. 31, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
TWR-2003 (Rel. 41, Last annotation update)
TWR-2003 (Rel. 41, Last annotation update)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Circumsporozoite protein precursor (CS).
Plasmodium berghei (strain Anka).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S07873; OZZOBK.
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PRO1303; CRCMSPRZOITE. SMART; SM00209; TSP1; 1. PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37776 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X17606; CAA35608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 29.9 tes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000884; TS
Pfam; PF00090; tsp_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
247
325
                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AA;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=5823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theologis A., Ecker J.R., Palma C.J., Federspiel N.A., Kaul S.,
Theologis A., Ecker J.R., Palma C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao G., Chen H., Cheuk R.F., Chin C.W.,
A. Chung W.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
B. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
A. Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Fujii C.Y.,
A. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A. Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P.,
A. Lingin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P.,
A. Lingin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sal H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
T. Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY.
                                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATURATION.
--- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
--- CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CY Columbia;
STRAIN-CY Columbia;
SIRAIN-CY Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RIKEN Arabidopais full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
1- TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                             Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.;
   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                       praper J., Scott K.;
Gametophytic and sporophytic expression of an anther-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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InterPro; IPR03882; Pistil_extensin.
Pfam; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60377; CAA42925.1; -.
EMBL; AC02472; ARF79900.1; ALT_SEQ.
EMBLs, AXO68847; AAL24235.1; -.
EMB.; S21961; S21961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=94004980; Pubmed~8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
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534
211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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FIFF WHILE WAS A SERVED BY A S
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33 PKPLPQQPPAPA-NQDQNSSQNTRLQPTPP----IPAPAPKPAAPPRPLDRESPGVEN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation protein 1 (Shank1) (GKAP/SAPAP interacting protein) (SPANT) (Synamon) (Somatostatin receptor interacting protein) (SSTR interacting protein) (SSTRIP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yao I., Hata Y., Hirao K., Deguchi M., Ide N., Takeuchi M., Takai Y.; "Symamon, a novel neuronal protein interacting with synapse-associated protein 90/postsynaptic density-95-associated protein."; J. Biol. Chem. 274:27463-27466(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 3), AND INTERACTION WITH DLGAP1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naisbitt S., Kim E., Tu J.C., Xiao B., Sala C., Valtschanoff J., Weinberg R.J., Worley P.F., Shang M., Shank, a novel family of postsynaptic density proteins that binds to the NWDA receptor/PSD-95/GKAP complex and cortactin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lim S., Naisbitt S., Yoon J., Hwang J.I., Suh P.G., Sheng M., Kim E., "Characterization of the Shank family of synaptic proteins. Multiple genes, alternative splicing, and differential expression in brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobaben S., Suedhof T.C., Stahl B.; "The G protein-coupled receptor CL1 interacts directly with proteins of the shank family.";
                                                                                                                                                                                                                                                                                        153 VPCPSPPKPPAPTPKPVPPHGPPPKPAP---APTP-----APSPKPAPSPP 195
                                                                                                                                                                                                                                                                    86 KLIPSVGSPASST -- PLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 4), AND INTERACTION WITH DLGAP1 STRAIN-Sprague-Dawley; MEDLINE-99360650; Pubmed-10433268;
                                                                                                                  14.2%; Score 146; DB 1; Length 534; 34.2%; Pred. No. 0.29;
                                                                                                                                                        45; Indels
                                                                              BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND
    POTENTIAL.
S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 2167 AA.
                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A. (ISOFORM 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99436166; PubMed-10506216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99419021; PubMed-10488079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20549637; PubMed=10958799;
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; Q9WU13; Q9WUE8;
511 PO
77 S
141 E
325 E
58007 MW;
                                                                                                                                    Local Similarity 34.2%
Les 39; Conservative
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  511 5
77
141 1
325 3
534 AA;
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  ACT_SITE
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                                                                            SEQUENCE
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Isold-O9WV48-5; Sequence=VSP_006076, VSP_006077;
TISSUE SPECTRICITY: Expressed only in brain (neuropil of cortex, CA1 region hippocampus and molecular layer of cerebellum.)
EVELOPMENTAL STAGE: Expression increases from low levels at birth to high levels at 3-4 weeks before dropping slightly in adulthood. Expressed in the cortex and the molecular layer of the cerebellum at postnatal day 7. Isoform 2 expression does not change during developmment of both cortex and cerebellum. Isoform 4 expression decreases significantly during development of cortex but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheng M., Kim E.;
"The Shank family of scaffold proteins.";
J. Cell Sci. 113:1851-1856 (2000).

J. Cell Sci. 113:1851-1856 (2000).

I cell Sci. 113:1851-1856 (2000).

The postsynaptic manages that interconnects receptors of the postsynaptic membrane including NMDA-type and metabotropic glutamate receptors, and the actin-based cytoskeleton. May play a role in the structural and functional organization of the dendritic spine and synaptic junction. Overexpression promotes maturation of dendritic spines and the enlargament of spine heads via its ability to recruit Homer to postsynaptic sites, and enhances presynaptic function.
                                                                                                                 INTERACTION WITH HOMER-1, AND SUBCELLULAR LOCATION.
MEDLINE=99360651; PubMed=10433269;
Tu J.C., Xiao B., Naisbitt S., Yuan J.P., Petralia R.S., Brakeman P.,
Doan A., Aakalu V.K., Lanahan A.A., Sheng M., Worley P.F.,
"Coupling of mcluk/Homer and PSD-95 complexes by the Shank family of
postsynaptic density proteins.";
Neuron 23:583-592(1999).
                  SUBUNIT: May homomultimerize via its SAM domain. Interacts with SPTANI, Homer-1 and DLGAP1/GKAP. Is part of a complex with DLG4/PSD-95 and DLGAP1/GKAP. Interacts with SSTR2 C-terminus via
                                                                                                                                                                                                                                                                                                                  Bockers T.M., Maneza M.G., Kreutz M.R., Bockmann J., Weise C.,
Buck F., Richter D., Gundelfinger E.D., Kreienkamp H.-J.;
"Synaptic scaffolding proteins in rat brain. Ankyrin repeats of the multidomain Shank protein family interact with the cytoskeletal protein alpha-fodrin.";
J. Biol. Chem. 276:40104-40112(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-21389514; PubMed-11498055;
Sala C., Piech V., Wilson N.R., Passafaro M., Liu G., Sheng M.;
"Regulation of dendritic spine morphology and synaptic function by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the PDZ domain (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; postsynaptic density of neuronal cells. Colocalizes with alpha-latrotoxin receptor 1.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=09WV48-2; Sequence=VSP_006072, VSP_006073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SHANK FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9WV48-3; Sequence=VSP_006074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     me=4; Synonyms=A;
IsoId=Q9WV48-4; Sequence=VSP_006075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9WV48-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                    MEDLINE=21523912; PubMed=11509555;
MEDLINE-20020275; PubMed-10551867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20267867; PubMed-10806096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shank and Homer.";
Neuron 31:115-130(2001).
                                                                                                                                                                                                                                                                                     INTERACTION WITH SPIAN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebellum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSEDSQTSLLSKPS -> QYRIVVKSSDFGDF (in
SIMILARITY: Contains 7 ANK repeats.
SIMILARITY: Contains 1 DPL//PHR domain.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                  Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_006076.
Missing (in isoform 5).
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S -> T (IN
S -> N (IN
R -> K (IN
A -> T (IN
S -> D (IN
S -> N (IN
                                                                                                                                                             InterPro; IPR002110; ANK.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001450; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SH3.
Pfam; PF00535; PDZ; I.
Pfam; PF00535; PDZ; I.
Pfam; PF00536; SAM; I.
Pfam; PF00518; SAM; I.
SMART; SM00228; PDZ; I.
SMART; SM00228; PDZ; I.
SMART; SM00448; SAM; I.
SMART; SM00428; SH3; I.
PROSITE; PS50088; ANK REPERAT; 3.
PROSITE; PS50088; ANK REPERAT; 3.
PROSITE; PS50016; PDZ; I.
PROSITE; PS50016; PDZ; I.
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POLY-PRO.
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PDZ.
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REPEAT 195 210 ANK
REPEAT 212 245 ANK
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PROSITE; PS50105; SAM_DOMAIN; 1.
                                                                                                                  EMBL; AF102855; AAD04569.2; -.
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245
245
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395
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                                                                      11;
                                                                                                                             1549 PLLVI,PPPAPSVDVDDGEFLFAEPLPPPLEFSNSFEKPESPLTPGPPHPL-PDPPSPATP 1607
                                                                                                                                                                                                                                                    98 TPLPP------DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTL 146
                                                                                                          6 HIONISNNKTERSTAPLNTOISALRNDP-----KPLPQQPPAPANQDQNSSQNTRLQ 57
                                                                                                                                                                             58 PTPPIPAPAP------KPAAPP-----RPLDRESPGVENKLIPSVGSPASS 97
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                             -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-1- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                        147 GENPD-----GLSQEQLEHRERS---LQTLRDIQRM--LFPDEKEFTGAQSGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-87089740; PubMed-2432395;
Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.;
Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.;
Eichinger D.J., Broth D.B., Pasmodium berghei: gene cloning and identification of the immunodominant epitopes.";
Mol. Cell. Biol. 6:3965-3972(1986).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTICEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 X 8 AA TANDEM REPEATS.
16 X 2 AA TANDEM REPEATS OF P-Q.
                                14.2%; Score 146; DB 1; Length 2167; 23.8%; Pred. No. 0.96; tive 35; Mismatches 82; Indels 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
2167 AA; 226333 MW; 3F478B5A7B18BA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E8068A6D11D9551B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Circumsporozoite protein precursor (CS). Plasmodium berghei.
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InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfan; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SWART; SW00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
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                                                                      56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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206
266
339 AA;
                                  Query Match
Best Local Similarity
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                                                                                             -----DPKPLPQQPPAPA 44
                                                                                                                                                                                     45 NQDQNSSQNTRLQPTPPIP--APAPKPAAPPRP--LDRESPGVENKLIPSVGSPA---SS 97
                                                                                                                                                                                                                                                                           98 TPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKA--PPPPPVSSGEPPTLGENP 150
                                                                                                                                                                                                                                                                                                                         156 DPAPPNANDP-APPN--ANDPAPPNAN-DPAPPNANDPPPPNPNDPAPPOGNNNP 206
  Length 339;
                                              66; Indels
Score 144.5; DB 1;
Pred. No. 0.24;
                                            51; Conservative 13; Mismatches
                                                                                          5 FHIQNISNNKT-ERSTAPLNTQISALRN----
                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October 15, 2003, 10:31:04 Job time: 25.4008 secs
14.1%;
29.1%;
  Query Match
Best Local Similarity
                                                 Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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October 15, 2003, 10:27:33; Search time 112.475 Seconds (without alignments) 445.097 Million cell updates/sec OM protein - protein search, using sw model Run on:

1 TIVSFHIQNISNNKTERSTA......LFPDEKEFTGAQSGGPQQNP 194 US-09-915-543-15_COPY_199_392 1028 Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

sp_archea:* sp_bacteria:* SPTREMBL_23:* Database :

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_archeap:* sp_rodent:* sp_virus:* sp_plant:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q39620 chlamydomon	Q9p4y9 neurospora	Q8w5k6 oryza sativ	Q9lvnl arabidopsis	036027 schizosacch	Q9p944 pneumocysti	O57580 gallus gall	Q96g51 homo sapien	Q9dgt6 turkey herp	Q8dgul synechococc	Q9rx57 deinococcus	Q39492 chlamydomon	Q9vzc2 drosophila	Q41805 zea mays (m	P70433 mus musculu	Q41645 volvox cart
a	039620	Q9P4Y9	Q8W5K6	Q9LVN1	036027	Q9P944	057580	096651	Q9DGT6	Q8DGU1	Q9RX57	039492	Q9VZC2	Q41805	P70433	041645
DB	10	m	10	10	m	ĸ	13	~*	12	16	16	10	Ŋ	10	11	10
% Query Match Length DB	473	876	1269	1307	574	1011	1151	816	2321	488	839	351	420	1188	802	464
% Query Match	17.3	16.4	16.3	15.9	15.8	15.8	15.8	15.7	15.6	15.6	15.6	15.4	15.4	15.4	15.4	15.3
Score	177.5	168.5	167.5	163	162.5	162.5	162.5	161.5	160.5	160	160	158.5	158.5	158.5	158	157.5
Result No.	П	7	3	4	S	9	7	80	σ	10	11	12	13	14	15	16

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74 RPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN-NRAVTPVSQGSNSSSADPKA 132

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	OBBAST A homo sapien OBBAST A mus musculu OBSUXZ arabidopsis OBSUXZ arabidopsis OBTII mysococcus O91164 arabidopsis	Q9akp3 rickettsla Q2o9693 trypanosoma Q9h6k5 homo sapien Q9lrm7 chlamydomon	Q8vin mycobacteri Q8vij6 mus musculu Q8uzb4 grapevine f Q9sbml volvox cart O15411 homo sapien Q96jk7 homo sapien	096191 homo sapien 062106 mus musculu 09gzhl caenorhabdi 08rwz arabidopsis 09c61 arabidopsis 09ary7 oryza sativ 02ace0 arabidopsis 09lqc5 arabidopsis 09lqc5 arabidopsis 08wxe0 homo sapien
Q9SPM0 Q9XDH2 Q9FPQ5 Q65530 Q22514	Q9BSV4 Q8K117 Q9SUX2 Q9RF11 Q9L,164	09AKP3 026963 09H6K5 08LRM7	Q8VKN/ Q8VIJ6 Q8UZB4 Q9SBM1 O15411 Q96JK7	Q96L91 Q62106 Q62L01 Q9CKH1 Q9CKS1 Q9CKS1 Q9ZUE0 Q9LQC5 Q9LQC5
12011	10 10 10 10	2 4 4 5 6	44 112	4 100 100 4 100 4 100 100 100 100 100 10
1315 763 386 731 326	637 883 956	602 964 616 1997	598 699 309 409 556 1157	3124 188 302 712 1201 273 731 1202
15.2 15.1 15.0 14.9	14.1 14.9 14.8 14.8	14.7	44444 4444 6.6.6.6.6	444444444 6.4.4.4.4.4.4.4.4.4.4.4.4.4.4.
156 154.5 154.5 153.5	153.5 152.5 152.5 152	151.5 151.5 151 151	150.5 150.5 150 150 150	1489 1489 1489 1489 1489 1489 159 159
11 11 11 12 12 12 13	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	30887	2 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~

ALIGNMENTS

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14 KTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPAPPP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Indels 27; Gaps
                                                                                                                                                                                                                                                     Woessner J.P., Molendijk A.J., van Egmond P., Klis F.M.,
Goodenough U.W., Haring M.A.;
"Domain conservation in several volvocalean cell wall proteins.";
Plant Mol. 26:947-960(1994).
EMBL; L29029; AAB53953.13.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                     Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBL_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 17.3%; Score 177.5; DB 10; Length 473; 1 Similarity 30.5%; Pred. No. 1.7e-05; 46; Conservative 19; Mismatches 59; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
38506131FAA674A4 CRC64;
                                                         01-NOV-1996 (TLEMBLrel. 01, Created)
01-NOV-1996 (TLEMBLrel. 01, Last sequence update)
01-MAR-2003 (TLEMBLrel. 23, Last annotation update)
                                PRT; 473 AA.
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                           MEDLINE-95093034; PubMed-8000007;
                                                                                                                                                                                                                                                                                                                                                                               SIGNAL 1 31 PU
CHAIN 32 473 PU
SEQUENCE 473 AA; 47532 MW;
                              PRELIMINARY;
                                                                                                         VSP-3 protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                              039620
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RESULT 1
Q39620
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NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LVN1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 PTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 KSPPAAAAAAAAAAPPPP------APAALTPAPP-----PPVTRKLT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 SPFSWLSRSSSKEQANPPPPPAAATAPRRNTASSVATLSSNPDGTLGKVDEEGNKNTLKD 325
 3 VSFHIQNISNNKT---ERS--TAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                       Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                  Neurospora crassa.
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 16.4%; Score 168.5; DB 3; Length 876; Best Local Similarity 30.1%; Pred. No. 0.00015; Matches 63; Conservative 24; Mismatches 61; Indels 61;
                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356834; -CAB92706.1;
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR00195; RabGAP_TBC.
Pfam; PR00566; TRC; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00164; TBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS50086; TBC_RABGAP; 1.
Hypothetical protein.
SEQUENCE 876 AA; 96784 WW; 5C8E11E6FD94EC5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TTEMBLrel. 20, Created)
01-MAR-2002 (TTEMBLrel. 20, Last sequence update)
01-MAR-2003 (TTEMBLrel. 23, Last annotation update)
Hypothetical 138.4 kDa protein.
0SJNBA0079B05.10 OR OSJNAA0079B05.2.
                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                        133 -----PPPPPVSSCEPPTLGENPDGLSQ 155
                                      433 SPSPAKKPSPPPPVEEGAPPPI-EGPPPMEE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 RFKOLRLREEGSAPTGDDDEKSSTPEEKE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 ---QLEHRER-SLQTLRDIQRMLFPDEKE 181
                                                                                                            PRT;
                                                                                                                                                                         Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                      B11B22.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8W5K6
                                                                                                            Q9P4Y9
                                                                                     RESULT 2
Q9P4Y9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQNTRLQPTPPIP---APAP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. x. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                 Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R., Rambo T., Saaki C., Henry D., Oates R., Simmons J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaese; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%; Score 167.5; DB 10; Length 1269; 32.6%; Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 1307;
                  Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01217; PRICHEXTENSN.
SMARY; SM0498; FH2; 1.
Hypothetical protein.
SEQUENCE 1269 Aa; 138432 MW; 262E546481B25CA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFD60BFB9669FA2A CRC64;
                                                                                                                                                                                                                                                                                            Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC079179; AAL31655.1; -.
EMBL; AC116601; AAM08709.1; -.
                                                                                                                       Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
GD|AAD23008.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones.";
DNA Res. 7:31-63(2000).
EMBL; AB0192218; BA496907.1; -.
InterPro; IPR003104; FH2.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF02181; FH2; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SMO498; FH2; 1.
SEQUENCE 1307 AA; 144545 MW; CFD60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GSNSSSADPKAPPPPVSSGEPPT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     657 GIGNKFPAPPPPPPPRSSSRTPT 680
                                                                                                                                                                                                                                                                                                                                                                                  Gramene; QBW5K6; -.
InterPro; IPR003104; FH2.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF02181; FH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20181125; PubMed=10718197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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              7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 RLQPTPP-----IPAPAPKPAAPPRLDRESPGVENKLIPSVGSPA-SSTPLPPDG 104
                                                                                                          66 APKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNS 125
                                                                                                                                662 NVASNLGQPARSPPPIS-----NSDKKPALPRPPPPPPPPPMOHSTVTKVPPPPP---- 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 IQNISNNKTERSTA----PLNTQISA----LRNDPKPLPQQPPAPANQDQ----NSSQNT 54
                                              9 NISNN--KTERSTAPLNTQISALRNDPKP-LPQQPPAPANQDQNSSQNTRLQPTPPIPAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 15.8%; Score 162.5; DB 3; Length 574;
l Similarity 30.9%; Pred. No. 0.00027;
50; Conservative 21; Mismatches 64; Indels 27; Gaps
                46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

-I. SIMILARITY: TO YEAST LAS17.

EMBL; AF038575; AAB925871:

EMBL; A289800, CAB11718.1:

GeneDB_SPombe; SPAC4F10.15c; -.

InterPro: IPR002965; EVH1.

InterPro: IPR002965; EVH1.
1 Similarity 29.9%; Fred. No. 0.00054; 46; Conservative 18; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 TGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 IPGRSAP---ALPPLGNASRTST--PPVPTPPSLPPSAPPSL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.

L -> V (IN STRAIN JS21).

CGESEFCA6A02F0E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                         126 SSADPKAPP------PPPVSSGEPPTLGE 148
                                                                                                                                                                                          Wiskott-aldrich syndrome protein homolog 1. WSP1 OR SPAC4F10.15C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY - PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00568; WHI; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00461; WHI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59605 MW;
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zankel T.C., Ow D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 3
248 2
574 AA;
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=JS21;
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Best Local S
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                  Matches
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                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 STAPLNTQISALRNDPKPLPQQPPAPANQ--DQNSSQNTRL---QPTP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 -----PILGENPDGLSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             780 PPKPTPQPTSEPAPQPTSESTSEP-TPRPPPQPTSEPTSEPTSEPTSEPSPSPQPTPQ 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Gaps
                                                                                                                                                                                                                               MEDLINE-20184731; PubMed=10721706;
Lee L.H., Gigliotti F., Wright T.W., Simpson-Haidaris P.J.,
Welnberg G.A., Haidaris C.G.;
"Molecular characterization of KEXI, a kexin-like protease in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-1889804464, PubMed=9365273;
Shimada K., Harata M., Mizuno S.;
"A nuclear matrix-associated high molecular mass nuclear antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.8%; Score 162.5; DB 3; Length 1011; 27.8%; Pred. No. 0.00046; tive 21; Mismatches 55; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1011 AA; 112021 MW; FBE472C8F65864E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                        01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kexin-like protease KEXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High molecular mass nuclear antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1151 AA
                                                                                                                                                                                                                                                                                                            Gene 242:141-150(2000).
-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
EMBL; AF093132; AAF32493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN 1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002884; P_domain.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF001483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF04886; PT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO0723; SUBTILISIN.
PRODOM; PD000717; P_domain; 1.
PROSTIE; PS00137; SUBTILASE_HIS; 1.
Protease.
                                                                                                                                       Pneumocystis carinii f. sp. muris.
                                                                                                                                                                                                                                                                                                                                                        MEROPS; S08.011; -. InterPro; IPR000209; Peptidase_S8. InterPro; IPR0006970; Pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                               Pneumocystis carinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                        Pneumocystis.
NCBI_TaxID=42066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                             09P944;
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                            Q9P944
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RESULT 6
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                                                                                                                                                                                                                                                                     3 PIPPPRNPPTP------PPAPSPAPAPAPAPAPAPPRPKWVPIAELHPAAPQPP 49
                                                                                                                                                                                                                                                                                                                                               33 PKPLPQQPPAPANQDQNSSQNTRLQPTP-PIPAPAPKPAAPPRP-----LDRESPGVE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.7%; Score 161.5; DB 4; Length 816; Best Local Similarity 32.1%; Pred. No. 0.00044; Matches 54; Conservative 7; Mismatches 64; Indels 43; Gaps
                                                                                                                                                                                                               39; Gaps
HMNA, of chicken and marked decrease of its immunoreactivity during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PSO1017: MAYK: 1.
PROSITE: PSO1051; MAYK: 1.
PROSITE: PSO1017: PROTEIN KINASE_ATP; 1.
PROSITE: PSO10107: PROTEIN KINASE_DOM; 1.
PROSITE: PSO10108: PROTEIN KINASE_ST: 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 816 AA; 88386 MM; 27729F831658CE38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                         Query Match 15.8%; Score 162.5; DB 13; Length 1151; Best Local Similarity 33.1%; Pred. No. 0.00052; Matches 45; Conservative 12; Mismatches 40; Indels 39;
                                                                                                                                     1151 AA; 109708 MW; 2403F6835F9A2AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        096651; 0969G1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mitogen-activated protein kinase 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Prot_kinase.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002290; Ser_thr_pkinase.
                 the progression of S phase.";
J. Cell Sci. 110:3303-3041(1997).
EMBL. D88440; BAA24137.1; -
InterPro; IPR003955; P.rich.extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC007992; AAH07992.1; -. EMBL; BC007404; AAH07404.1; -. EMBL; BC030134; AAH30134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase; 1.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     95 SPPDGPKAPSGAGEAE 110
                                                                                                                                                                                                                                                                                                                                                                                                 142 EPPTLGENPDGLSQEQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pancreas, and Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC009963; AAH09963.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                         1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P24941; 1BUH.
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                                                                                                                         1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.
                                                                                                                                             SEQUENCE
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Q96G51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 PLPPDGTGP-----NSTPNNRAVTPVSQGSNSS----SADPKAPP--PPPVSSGEPPTL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 NRASEROLA--DTAASALR-APSPVFWSAFDSRYPHLAPANOSNSDPLCPETSTASAOIL 297
                                   577 RPAAPALTSVPAPAPAPTPTPTPVQPTSPPGGPVAQPTGPQPQSAGSTSGPVPQPACPPP 636
                                                                       64 APAPKPAAPPRPLDRESPG-----VENKLIPSVGSPASSTP-----LPPDGT 105
                                                                                               12 NNKTERSTAPLNTQISALRNDPKPL-----PQQPP-APANQD-----QNSSQNTRL- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ---QPTPPI---PAPAPKPAAP----PRPLDRESPGVENKLIPSVGSPAS----ST 98
17 RSTAPLNTQISALRNDPKPLP-------QOPPAPANQDQNSSQNTRLQPTPPIP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tulman E.R., Afonso C.L., Lu Z., Esak L., Rock D.L., Kutish G.F.; "The genome of a very virulent Marek's disease virus."; J. Virol. 74:7980-7988(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fulman E.R., Afonso C.L., Lu 2., Zsak L., Rock D.L., Kutish G.F.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF243438; AAG14244.1;
EMBL; AF243438; AAG14273.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unery Match 15.6%; Score 160.5; DB 12; Length 2321; Best Local Similarity 32.4%; Pred. No. 0.0015; Matches 60; Conservative 21; Mismatches 53; Indels 51;
                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
RS1 immediate-early gene transactivator ICP4-like protein (RS1 immediate-early gene transactivator-like protein).
MDV084 OR MDV100.
                                                                                                                                                   106 G--PNS----TPNNRAVTPVSQGSNSSSADPKAPPPPVSSGEPPTLG 147
                                                                                                                                                                      697 GGAPQSSMSESPDVNLVT--QQLSKSQVEDPL----PPVFSGTPKGSG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005205; Herpes_ICP4_C.
InterPro; IPR002206; Herpes_ICP4_N.
InterPro; IPR002966; Herpes_ICP4_N.
Pfam; PF03585; Herpes_ICP4_C; 1.
Pfam; PF03584; Herpes_ICP4_N; 1.
PRIWTS; PR01217; PRICHEXTENS.
SEQUENCE 2321 AA; 252959 WW; FF130EB0C4503003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Turkey herpesvirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 AA.
                                                                                                                                                                                                                                                                                  PRT; 2321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Md5;
MEDLINE=20392152; PubMed=10933706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                              RESULT 9
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ID Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 -SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPP---PPVSSGEPPT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                       Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Tomplete genome structure of the thermophilic cyanobacterium DNA Res. 9:123-130(2002).

EMBL: AP005376; BAC09774.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann K.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                           15.6%; Score 160; DB 16; Length 488; 33.3%; Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                             Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002903; F. L.C. PRINTS; PR01217; PRICHEXTENSN.
Hypothetical protein; Complete proteome.
GROUGHER 839 AA; 79759 MW; 386C2CD0CFEFF4DE CRC64; Fondt
                                                                                                                                                                                                                                                                                                                                        Kinase; Complete proteome.
SEQUENCE 488 AA; 52553 MW; 71287B898A6DBB09 CRC64;
             01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ol-MAY-2000 (TrEMBLrel. 13, Created)
ULMAR-2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical protein DR0458.
                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           839 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                          MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20036896; PubMed=10567266;
                                                              Serine/threonine protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 286:1571-1577(1999).
EMBL; AE001904; AAF10038.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR0458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M.;
                                                                             rrr2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RX57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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Length 839;

Score 160; DB 16; Pred. No. 0.00059;

15.6%; 31.3%;

Query Match Best Local Similarity

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282 GSVVPEATVPESSTPAAPSAQTPPTPTRETAQTEASPAAPNSSAAAPNEPASEPV-AGRP 340
                                              85 NKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTPVSQGS-NSSSADPKAPPPPVSSGEP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 SVYNNCIDTRPAPYNCSTFNVTSVITPTPSPSPSPSPSPSPSPSPSPKASPSPSPKASPS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 P-PIPAPARPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPPDGTGPNSTPNNRAVTP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 PSPKASPSPSPKASPAPSPQPSPTPSPKASPVASPQQSPTPSPRPSPTPSPTP----SP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                           33 PKP-LPQQPPAPANQDQNSSQNTRLQP---TPPIPAPA---PKPAAP-PRPLDRESPGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 NISNNKTERSTAPLNTQ----ISALRNDPKPLPQQPPAPANQDQNS-----SQNTRLQPT
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=UTEX 10;
MDEDLINE=25093034; PubMed=8000007;
WOESSER J.P., Molendijk A.J., van Egmond P., Klis F.M.,
Goodenough U.W., Haring M.A.;
"Domain conservation in several volvocalean cell wall proteins.";
                                                                                                                                                                                                                                                                                                                                                  Chlamydomonas eugametos.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.4%; Score 158.5; DB 10; Length 351; 30.9%; Pred. No. 0.00032; Live 15; Mismatches 71; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda: Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                          144 PTLGENPDGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGG 189
                                                                                                                                                                     341 GTAASSPESASPVTVTPRGET------PDTAASAGTPSAG 374
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70AD2EFF7C74BB68 CRC64;
                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
    79;
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPKASPPSASPSASPSLSPKVSPSTPPT
                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. 26:947-960(1994).
EMBL: L29028; AAB53954.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created) 01-OCT-2002 (TrEMBLrel. 22, Last seq 01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonadaceae; Chlamydomonas
   13;
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32 351 PK
351 AA; 35310 MW;
                                                                                                                                                                                                                                                                            01, 01, 23,
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   Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                           (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                      WP6 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VZC2; Q8S247;
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01-MAR-2003
52;
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SEQUENCE
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Matches
                                                                                                                                                                                                                   RESULT 12
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91 VG-----SPASSTPLPPDGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 YGPPQTPPPRPPPQPTPSAPAPPSYGPPQTPPPPPPPPPPPSAPAPSYGPPQPPAPQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 PKPLPQQPPAPANQDQNSSQNTRLQPTPPIPAPA--PKPAAPPRPLDRESPGVENKLIPS
                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Carape M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCBL Clade; Panicoideae; Andropogoneae; Zea.
                 Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEAUGHER): TISSUE-POLIER;
Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.;
Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.;
"Pex genes: pollen-specific genes with extensin-like domains.";
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, 234465; CAR84230.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                            15.4%; Score 158.5; DB 5; Length 420; 29.6%; Pred. No. 0.00038; Live 11; Mismatches 64; Indels 25
                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR003481; AAL48746.1; -.
EMBL; AX01124; AAL48746.1; -.
FlyBase; FBR0035544; CG15021.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; Prich_extensn.
PRINTS; PR01217; PRICHEXTENSIN.
PRINTS; PR01217; PRICHEXTENSIN.
SEQUENCE 420 AA; 42947 MW; 96D62FFDC9F996E1 CRC64;
                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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1188 AA; 120981 MW; 2C77C7F8D7130149 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 SGEPPTLGENPDGLSQEQLEHR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 PPSPPSPQPGPEYLPPDQPKPR 200
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PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                    SEQUENCE FROM N.A.
                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                        STRAIN-Berkeley;
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                                                                                                                                                                                                                                                         Celniker S.;
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The state of VaSP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";

"Mena, a relative of VaSP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";

"Cell 87:227-239(1996).

"Cell 87:22
                                                                               7;
                                                                                                                                                                                        1021 PPPPVKSPPPPAPVSSPPPVKS---PPPPAPVSSPPPPVKSPPPAPISSPPPPVKSPP 1077
                                                                                                                                                                                                                                                                               69 P-----AAPPRPLDRESPGVENKLIPSVGSPASSTPLP---PDGTGPNSTPNNRAVTPV 119
                                                                                                                                     14 KTERSTAPLNTQISALRNDPKPLP--QOPPAPANQDQNSSQNTRLQP---TPPIPAPAPK 68
Query Match
Best Local Similarity 32.0%; Pred. No. 0.0011;
Matches 49; Conservative 17; Mismatches 68; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ARG.
PHOSPHORYLATION (BY CAPK AND CGPK) (BY
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PHOSPHORYLATION (BY CAPK AND CGPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MISSING (IN ISOFORM MENA AND ISOFORM
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CIFC -> VFYL (IN ISOFORM MENA++).
MISSING (IN ISOFORM MENA).
592BB975EE20F77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P70433 PRELIMINARX; PRT, 802 AA.
P70433; P70430; P70431; P70432;
D1-FEB-1997 (TrEMBLEI. 02, Created)
01-FEB-1997 (TrEMBLEI. 02, Last sequence update)
01-FBF-2003 (TrEMBLEI. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1078 PPAPVSSPPPPVKSPPPPAPVSSPPPPIKSPPP 1110
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SEQUENCE FROM N.A., AND CHARACTERIZATION.
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POLY-PRO.
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POLY-PRO.
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SWART; SWO0461; WRABD; 1.
SWART; SWO0461; WRALF, 1.
Alternative splicing; Phosphorylation.
DOMAIN 442 464
DOMAIN 542 552 POLY-PRO.
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MEDLINE=97015079; PubMed=8861907;
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259
802 AA;
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ENAH OR MENA.
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----DRESPGVENKLI------PSVGSPASS-TPLPPD-GTGPNSTPNNRAV- 116
                                                                                                                  348 NKNSRPSSPVNTPSSQPPAAKSCAWPISNFSPLPPSPPIMISSPPGKATGPRPVLPVCVS 407
                                                                                                                                                                                     468 LSHCGSQASPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGDSSASEPGLQAAS 527
                                                                                                                                                           34 KPLPQQPPAPANQDQN-----SSQNTRLQPTPPLPAPAPKPAAPPRPL----
                                                    Gaps
                                                88;
      15.4%; Score 158; DB 11; Length 802; 26.3%; Pred. No. 0.00079; ive 15; Mismatches 62; Indels 8
                                                                                                                                                                                                                                                                                                                ----TPVSQGSNSSSADPKAPPPPVSSGE-----PPTLGENP 150
                                                                                                                                                                                                                                                                                                                                                    528 QPAESPTPQG--LVLGPPAPPPPPPPPPSGPAYASALPPPPGPPP 569
                                                                                13 NKTERSTAPLNT-------QISALRNDP-----
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Query Match 15.49
Best Local Similarity 26.39
Matches 59; Conservative
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October 15, 2003, 10:27:32 ; Search time 21.5175 Seconds (without alignments) 258.182 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          178
1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                         US-09-915-543-15_COPY_349_383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

SUMMARIES

Description	CHOR Select Choracter Selection Company	Human BCL9 homolog	Mouse beta-catenin	Mouse beta-catenia	Human beta-catenin	Haman leaf nemer	Drosophila melanog	D. melanogaster lo	Aspergillus fumiga
ΩI	AAB71229	ABB11808	AAU78461	AAU78460	AAU78463	AAB71230	ABB58779	AAB71228	ABJ25853
DB .	23	22	23	23	23	23	22	23	24
% Query Match Length DB .ID			320						
& Query Match	100.0	100.0	61.2	61.2	60.1	60.1	37.1	37.1	32.3
Score	178	178	109	109	107	107	99	99	57.5
Result No.	Н	7	3	4	2	9	7	80	O

Aspergillus fumiga Drosophila melaanog Human protein sequenchuman ovarian canc Amino acid sequenchuman oacid sequenchuman GTP-binding Human GTP-binding Human Ovarian canc Murine bHLM transcr Human bHLM transcr Thermus thermophil Human bHLM transcr Human bHLM transcr Human bECTECTOR GACTOR AGENTAL	
24 ABJ26453 22 ABB65502 22 AAB65073 23 AAG63852 22 AAG63852 22 AAG68362 22 AAG68362 22 AAG68362 22 AAG69628 23 ABG96281 23 ABG96284 22 AAG69628 22 AAG69628 22 AAG696744 22 AAG696744 22 AAG696744 22 AAG696744 22 AAG9946 22 AAG9946 22 AAG9946 22 AAG9946 22 AAG99965 22 AAG99965 22 AAG99965 22 AAG99965 22 AAG99965 23 AAG99965 24 AAG99965 25 AAG99965 26 AAG99965 27 AAG99965 28 AAG99965 28 AAG99965 28 AAG99965 28 AAG99965 28 AAG99965 28 AAG99965 29 AAG9965 20 AAG99965 21 AAG9965 21 AAG99965 22 AAG99965 23 AAG99965 24 AAG9965 25 AAG99965 26 AAG99965 27 AAG99965 28 AAG99965 28 AAG9965 28 AAG9967 28 AAG9967	ALIGNMENTS
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Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg; tissue proliferation; tumour; cytostatic; cellular disorder; colon; blood disorder; cancer; breast; head and neck cancer; brain; thyroid; medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                                                                                                                                                                                                                                                                                               Basler K, Brunner E, Froesch B, Kramps T, Peter O;
                                                                                       Human legless homologue 1gs/bc19 protein.
                     AAB71229 standard; Protein; 1426 AA.
                                                                                                                                                                                                                                              27-JUL-2001; 2001US-0915543.
                                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-221502P.
                                                                    (first entry)
                                                                                                                                                                                                                                                                                         (BASL/) BASLER K.
(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
(KRAM/) KRAMPS T.
                                                                                                                                                                                              US2002086986-A1.
                                                                                                                                                                                                                                                                                                                                          PETER O.
                                                                                                                                                                          Homo sapiens.
                                                                  18-NOV-2002
                                                                                                                                                                                                                       04-JUL-2002.
                                           AAB71229;
                                                                                                                                                                                                                                                                                                                                          (PETE/)
            AAB71229
RESULT 1
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factor;
                                                                                                                                                                                                                                                                                               This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (1gs) protein, a downstream component of the Wnt/Wingless (Wnt/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wnt pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; growth factor inhibin; cytokine; cell proliferation; tissue growth; immunomodulator; activin; inhibin; chemctaris; chemckinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cepeneration; wound healing; infection; immune disorder; antiastentic; drug screening; gene therapy; antiniflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial;
                                                                                                                            Novel polypeptide useful in therapeutic method for treating disorders of cell fate such as cell differentiation or cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 178; DB 23;
100.0%; Pred. No. 8.6e-16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BCL9 homologue, SEQ ID NO:2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB11808 standard; peptide; 1435 AA
                                                                                                                                                                                                                                   Example II; Fig 8B; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antifungal; vulnerary; antiulcer
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 35; Conservative
                               WPI; 2002-635689/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1426 AA;
                                                               N-PSDB; AAF88467
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NAME OF THE PART O
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Tang YT, Liu C, Drmanac RT;

(HYSE-) HYSEQ INC

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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA00225-ABA09574 represent nucleic acids encoding them. The sequences ABA00225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. Or the invention, atthough novel, many of the nucleotides of the invention although novel, many of the polypeptides of the invention although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable bological activities, and hence potential therapeutic applications. The polypeptides of the invention activities, including officer activity; and hence there activities including officer activities, and hence them activities; stem cell growth activity; inmunomodulatory activity; activit, tissue growth activity; immunomodulatory activities; receptor or linhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions and unclearing medical streaming, bone disorders (e.g., myeloid or lymphoid cell or proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with healing (e.g., of burns, incisions and ulcers), while those with complete stem cells in culture to give rise to neuroepithelial cells and pundal incidents and benefice and benefice to be promote cell growth. For example, such polypeptides my be used to browner describered benefices and pulpapelides but gament pulpapelides and pulpapelides but gament and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease or accidental damage. The polypeptides and nucleotid may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; beta-catenin nuclear localised protein; cancer; gene therapy; EST; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 178; DB 22;
Pred. No. 8.7e-16;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse beta-catenin nuclear localised protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                              Claim 20; Page 256-257; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU78461 standard; Protein; 320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                          e.g. arthritis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2002 (first entry)
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WPI; 2001-457740/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                    N-PSDB; ABA09052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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Gaps

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us-09-915-543-15_copy_349_383.rag

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* beta-catenin nuclear localised protein for diagnosis and treatment diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                      nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence human beta-catenin nuclear localised protein #2.
                                      The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with
                                                                                                                                                                                                     Length 1494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 23; Length 738;
Pred. No. 3e-06;
                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; beta-catenin nuclear localised protein; cancer; gene therapy; EST; expressed sequence tag.
                                                                                                                                                                                                 Score 109; DB 23;
Pred. No. 3.5e-06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta-catenin nuclear localised protein #2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 102-105; 113pp; Japanese.
                                                                                                                                                                                                                                                                                        1 DGLSQEQLEHRERSLQTLRDIQRML 25
     Claim 1; Page 81-88; 113pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GLSQEQLEHRERSLQTLRDIQRML 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78463 standard; Protein; 738 AA.
                                                                                                                                                                                                 61.2%;
84.0%;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-2001; 2001WO-JP08140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-2000; 2000JP-0287876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-330014/36.
N-PSDB; ABK47638.
                                                                                                                                                               1494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adachi
                                                                                                                                                                                                                Local Similarity
Les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200224738-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Best Local Simil
Matches 21; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78463;
                                                                                                                                                                                                                                                                                                     394
                                                                                                                                                                 Sequence
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                                                                                                                                                                                                 Query Match
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ID AAU7
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                                                                                                                                                                                                                                                           New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New beta-catenin nuclear localised protein for diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                             The invention relates to a beta-catenin nuclear localised protein and DNA encoding the protein. The protein and encoding DNA are applicable in diagnosis and treatment of diseases associated with nuclear localisation of beta-catenin e.g. cancer, including gene therapy. The present sequence represents the amino acid sequence of mouse beta-catenin nuclear localised protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109; DB 23; Length 320;
Pred. No. 6.3e-07;
Wismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; beta-catenin nuclear localised protein; cancer; gene therapy; EST; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse beta-catenin nuclear localised protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 EGLSKEQLEHRERSLQTLRDIERLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                                                                                Claim 2; Page 91-92; 113pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU78460 standard; Protein; 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.2%;
84.0%;
                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                  19-SEP-2001; 2001WO-JP08140
                                                                                                     22-SEP-2000; 2000JP-0287876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                          Adachi S;
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N-PSDB; ABK47631.
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Les 21; Conserv
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                                                                                                                                                                                                                          N-PSDB; ABK47632
WO200224738-A1
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                                                                                                                                                                           Akiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Gaps

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(first entry)
26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (49s) protein, a downstream component of the Wilfyless (WilfyMg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and growth of many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancers caused by over-stimulation of the Wint pathway, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the human legless (49s) protein homologue higs-I described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide useful in therapeutic method for treating disorders of cell fate such as cell differentiation or cell proliferation
                                                                                                                           Legless; human; lgs; Wnt/Wingless signaling pathway; Wnt; Wg;
tissue proliferation; tumour; cytostatic; cellular disorder; colon;
blood disorder; cancer; breast; head and neck cancer; brain; thyroid;
medulloblastoma; skin cancer; tissue regeneration; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Peter 0;
                                                                                                       Human legless homologue hlgs-1 partial protein.
                                                                                                                                                                                                                                                                                                                                                                         Froesch B, Kramps T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 GLSKEQLEHRERSLQTLRDIERLL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GLSQEQLEHRERSLQTLRDIQRML 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB58779 standard; Protein; 1429 AA.
                                   AAB71230 standard; Protein; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example II; Fig 10B; 41pp; English.
                                                                                                                                                                                                                                                         27-JUL-2001; 2001US-0915543.
                                                                                                                                                                                                                                                                                28-JUL-2000; 2000US-221502P.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Basler K, Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-635689/68.
                                                                                                                                                                                                                                                                                                      (BASL/) BASLER K.
(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
(KRAM/) KRAMPS T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1115 AA;
                                                                                                                                                                                                                                                                                                                                                     (PETE/) PETER O.
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF88468
                                                                                                                                                                                                           US2002086986-A1.
                                                                                                                                                                                      Homo sapiens.
                                                                                18-NOV-2002
                                                                                                                                                                                                                                  04-JUL-2002.
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                                                         AAB71230;
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Matches
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             RESULT 6
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                        AAB71230
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furugs. The invention discloses genomic DNA sequences (ABLIGIT6-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                       Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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Drosophila melanogaster polypeptide SEQ ID NO 3129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB71228 standard; Protein; 1464 AA
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                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                  Drosophila melanogaster.
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ABJ26453;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fungicide, cytostatic, essential gene, Aspergillus fumigatus; infection, cancer, contamination, biofilm; antibody; immune response.
                                                                                                                                                                                                                                                     This invention describes a novel polypeptide sharing one or more homologous amino acid domains with the legless (19s) protein, a downstream component of the Witt/Wingless (Wit/Wg) signaling pathway involved in the formation and maintenance of spatial arrangements and proliferation of tissues during development, and in the formation and proliferation of tissues during development, and in the formation of provided many human tumours. The products of the invention have cytostatic activity and can be used to treat cellular disorders, blood disorders and cancerous condition is colon, breast, head and neck, brain, where the cancerous condition is colon, breast, head and neck, brain, thyroid, medulloblastoma or skin cancer. The product could also be used to promote tissue regeneration and repair. This sequence represents the prosphila melanogaster (fruitfly) legless (19s) protein described in
                                                                                                                                                                                               Novel polypeptide useful in therapeutic method for treating disorders of cell fate such as cell differentiation or cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 37.1%; Score 66; DB 23; Length 1464; Local Similarity 31.4%; Pred. No. 3.2; Lonservative 10; Mismatches 14; Indels C
                                                                                                                                       Froesch B, Kramps T, Peter O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus essential gene protein #511.
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515 ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ25853 standard; Protein; 603 AA.
                                                                                                                                                                                                                                  Example II; Fig 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 the disclosure of the invention.
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2001US-295890P.
2001US-303899P.
2001US-316362P.
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                       27-JUL-2001; 2001US-0915543
                                             28-JUL-2000; 2000US-221502P
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                                                                                                                                         Basler K, Brunner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus fumigatus
                                                                                                                                                               WPI; 2002-635689/68.
                                                                   (BASL/) BASLER K.
(BRUN/) BRUNNER E.
(FROE/) FROESCH B.
(KRAM/) KRAMPS T.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1464 AA;
                                                                                                                 (PETE/) PETER O.
                                                                                                                                                                          N-PSDB; AAF88466
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31-AUG-2001;
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05-JUN-2001;
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 04-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ2585
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a blofilm comprising A. fumigatus or inhibit formation on a surface of a blofilm comprising A. fumigatus for host tissues in which the pathogenic expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having with DNA sequences of other related or distant pathogenic organisms to identify and/or incompanies. For selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-DNA antibodies or to elicit annibodies, as an encompanies or the other repression contains an incoher incoher immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a protein of one of the essential genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.
                                                                                                                                                                                                                                             New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject
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                                                                                      Lemieux SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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                                                                                  Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus essential gene protein #1111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 18;
; Mismatches
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31.4%; Pred. No. 18
ative 11; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABJ26453 standard; Protein; 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002WO-US13142.
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Les 11; Conservative
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus.
                                                                                                                                                                    WPI; 2003-093124/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200286090-A2.
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                                                                                                                                                                                                                                                                                                                                                                                           e.g. cancer
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27-SEP-2001.
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AAB95073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to
                                                                                                                                                                                                                                                                                               essential genes of Aspergillus fundatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fundatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fundatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an
                                                                                                                                                                                          Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  The invention relates to novel purified or isolated nucleic acids of
                                                                                                                    Lemieux SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen to raise anti-DNA antibodies or to elicit another immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.3%; Score 57.5; DB 24; Length 618; Best Local Similarity 31.4%; Pred. No. 19; Matches 11; Conservative 11; Mismatches 10; Indels 3,
                                                                                                                                                                              New purified or isolated nucleic acids of essential genes of
                                                                                                                   Hu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 17298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zamudio C, Eroshkin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB63502 standard; Protein; 1294 AA
                                                                                                                                                                                                                                                      Disclosure; Page -; 175pp; English.
            27-APR-2001; 2001US-287066P.
05-JUN-2001; 2001US-295890P.
09-JUL-2001; 2001US-303899P.
23-APR-2001; 2001US-285697P.
                                                         31-AUG-2001; 2001US-316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002 (first entry)
                                                                                      (ELIT-) ELITRA PHARM INC
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                                                                                                                   Tishkoff D,
                                                                                                                                                 WPI; 2003-093124/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               618 AA;
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                                                                                                                                                                                                                            e.g. cancer
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                                                                                                                    Jiang B,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furges. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 17298; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 1294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T, Isogai T, Nishikawa T, Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 68;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:16943.
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                                                                                                                                                                                                            Li PWD,
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
23-MAR-2001; 2001WO-US09231.
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                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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Matches 10; Conservative
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                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                 WPI; 2001-656860/75
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                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                   N-PSDB; ABL07605
                                                                                                                                                                                                                                                                                                                                                                                                                      interactions -
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Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; brachimer's disease; Parkhnson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length converse the primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13642 to AAH13632 represent human amino coid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of injonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a bilgonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence, and the combination of the 5'-end sequence, and sequence is selected from those defined in
                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                Claim 8; SEQ ID 16943; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
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Best Local Similarity 52.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the present invention.
Sugiyama T,
                                       WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200271928-A2.
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Ishii S,
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the expression level of a marker in a patient sample and the normal level of expression level of a marker in a patient sample and the normal level of expression level of a marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the cancer is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having a familial history of ovarian cancer (e.g. patients having a familial history of ovarian cancer.). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and disorders (e.g. bacterial or viral meningitis, batchemers (e.g. bacterial or viral meningitis), connective tissue disorders (e.g. nortuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disorders (e.g. ischaemic heart disorders (e.g. ischaemic heart disorders (e.g. ischaemic cancer, monitoring the progression of ovarian cancer, connecting the ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer or at risk of developing ovarian cancer. The chibiting ovarian cancer or at risk of developing ovarian cancer markers described in the particular cancer or at risk of developing ovarian cancer markers
                                                                                                                                                                                                                                                                                                                               Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new method for assessing whether a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTPase activating protein; GTPAP1; cell signalling; immune disorder; cell proliferative disorder; cancer; colon cancer; arteriosclerosis; diabetes; psoriasis; hepatitis; multiple sclerosis; gene therapy.
                                                                                                                                                                          E, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
Lu K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human GTPase activating protein GTPAP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 134-135; 481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GLRTEGLFRRSASVQTVREIQRL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG63851 standard; Protein; 433 AA.
                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                       26-SEP-2001; 2001US-324967P.
26-SEP-2001; 2001US-325102P.
26-SEP-2001; 2001US-325149P.
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2001US-311732P
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nes 12; Conserv
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10-AUG-2001;
                       9-SEP-2001;
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A substantially purified GTPase activating protein useful for treating or preventing cell signalling, immune and cell proliferative disorders, including cancer especially colon cancer -
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                                                                                                                                                                                                                 /note= "potential protein kinase phosphorylation
    site for casein kinase II"
                                                                                                                                                                                                                                                                                                                             /note= "potential protein kinase phosphorylation
    site for casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                        "potential protein kinase phosphorylation site for protein kinase C"
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site for casein kinase II"
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    site for casein kinase II"
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site for tyrosine kinase"
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                                                                       /note= "potential protein kinase phosphorylation
                                                                                                                    "potential protein kinase phosphorylation
site for tyrosine kinase"
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    site for protein kinase C"
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382
                                                                                       site for tyrosine kinase'
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                                                                                                                                                                                                                                                               "GTPase-activator domain"
                                                                                                                                                                                                                                                                                               "GTPase-activator domain"
                                       Location/Qualifiers
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             Homo sapiens
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Baughn MR;

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arteriosclerosis, diabetes, psoriasis, hepatitis and multiple sclerosis. GTPAP1 polynucleotides are also useful for gene therapy treatments of the diseases.
                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "potential protein kinase phosphorylation site for tyrosine kinase"
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site for casein kinase II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential protein kinase phosphorylation site for tyrosine kinase"
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    site for protein kinase C"
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site for casein kinase II"
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    site for protein kinase C"
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    site for protein kinase C"
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    site for tyrosine kinase"
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                                                                                                                                                                                                                                                                                                                 Amino acid sequence of human GTPase activating protein GTPAP2.
                                                                                  Length 433;
                                                                                                            7; Indels
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                                                                                  DB 22;
28;
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                                                                                Score 55;
Pred. No.
                                                                                                                                                     224 GLRTEGLFRRSASVQTVREIQRL 246
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                     2 GLSQEQLEHRERSLQTLRDIQRM 24
                                                                                                                                                                                                                                   AAG63852 standard; Protein; 433 AA.
                                                                                30.9%;
52.2%;
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Best Local Similarity 52.28
Matches 12; Conservative
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Ouery Match 30.9%; Score 55; DB 22; Length 433; Best Local Similarity 52.2%; Pred. No. 28; Matches 12; Conservative 4; Mismatches 7; Indels

Search completed: October 15, 2003, 10:30:24 Job time: 23.5175 secs

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56, Appl
23210, A
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Sequence 30, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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209.113 Million cell updates/sec
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                                                                               October 15, 2003, 10:27:32; Search time 7.08171 Seconds
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                            1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
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US-09-515-91A-25843
US-09-651-656-15
US-09-651-656-15
US-09-252-991A-24834
US-09-252-991A-24834
US-09-247-373B-54
US-09-247-373B-54
US-09-342-749A-2
US-09-186-276B-56
US-09-107-278-226
US-09-107-5328-2226
US-09-107-5328-2256
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Listing first 45 summaries
                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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19252, A
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                              US-09-252-911A-18906
US-09-252-991A-31012
US-09-252-991A-23336
US-09-252-991A-16908
US-09-252-991A-16908
US-08-466-390-4
US-08-467-781-4
US-08-467-781-4
US-08-467-781-4
US-08-467-781-4
US-08-467-781-4
US-08-452-294-1
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US-08-858-207A-395
US-09-252-991A-19252
US-08-690-011A-34
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; OTHER INFORMATION: Incyte ID No. 6509155 g6572185
US-09-507-765-32
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Petent No. 6509155
GENERAL INFORMATION:
APPLICANT: Kinger, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Yue, Henry
APPLICANT: We, Henry
APPLICANT: Bughn, Mariah R.
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
CURRENT APPLICANT APPLICATION NUMBER: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGram
SEQ ID NO 30
                                                                                                                                                                                                                                                                                Sequence 32, Application US/09507765
Fatent No. 6509155
GENERAL INFORMATION:
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: GTPASE ACTIVATING PROFEINS
FILE REFERENCE: PC-0010 US
CURRENT APPLICATION NUMBER: US/09/507,765
CURRENT FILLING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOSTWARE: PERL PROGRAM
PCT-US95-04682-3
US-09-107-532A-5104
US-09-107-532A-3753
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226.1
225.0
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Sequence 11, Appl Sequence 5226, Ap Sequence 22579, A Sequence 22746, A

Sequence 29240, A Sequence 31361, A Sequence 3159, Ap Sequence 3, Appli

US-09-252-991A-22746 US-09-252-991A-29240 US-09-252-991A-31361 US-09-134-001C-3159 US-08-227-536-3

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                  6; Indels
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                                                                                          5 QEQLEHRERSL------QTLRDIQRMLFPDEKEF 32
             9; Mismatches
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; Patent No. 6365355
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             13; Conservative
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US-09-651-656-15
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LENGIH: 819
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Patent No. 6551795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: US 60/074,788
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                                                                                                                                                                                                                                                                                                     Ouery Match 30.9%; Score 55; DB 4; Length 433; Best Local Similarity 52.2%; Pred. No. 9.1; Matches 12; Conservative 4; Mismatches 7; Indels
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US-09-507-765-31
                                                                                                                         NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. 6509155 3068538CD1
US-09-507-765-30
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APPLICANT: Klinger, Tod M.
APPLICANT: Stewart, Filzabeth A.
APPLICANT: Stewart, Filzabeth A.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
FILE REFERENCE: PC-0010 US
CURRENT APPLICATION NUMBER: US/09/507,765
CURRENT FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 333
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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SEQ ID NO 31
LENGTH: 433
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Best Local Similarity
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US-09-252-991A-25843
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LENGTH: 1242
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                                                                                          FEATURE:
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Sequence 15, Application US/09651656
; Patent No. 6340516
; Patent No. 6340516
; Patent No. 6340516
; GENERAL INFORMATION:
; APPLICANT: IMCUTHEN-MALONEY, SANDRA
; APPLICANT: IMCUTHEN-MALONEY, SANDRA
; APPLICANT: IMCRENCE INTERMONE DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
; FILE REFERENCE: 11-10689
; CURRENT APPLICATION NUMBER: US/09/651,656
; CURRENT FILING DATE: 2000-03-28
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NOS: 106
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APPLICANT: MCCUTENTEN-MALONEY, SANDRA
APPLICANT: MCCUTENTEN-MALONEY, SANDRA
APPLICANT: LAMRENCE LIVERMORE MATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MUTANIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: 1L-10284
CURRENT APPLICATION NUMBER: 05/99/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN Ver. 2.1
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US-09-252-991A-23906
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APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANTEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZIMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-01-10
PRIOR APPLICATION NUMBER: 08/924,747
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                              Query Match 28.4%; Score 50.5; DB 4; Length 354; Best Local Similarity 40.0%; Pred. No. 30; Matches 14; Conservative 6; Mismatches 8; Indels 7
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APPLICANT: Joergensen, Steen T.
APPLICANT: Christensen, Christina L.
APPLICANT: Christensen, Tina
APPLICANT: Kristensen, Tina
TITLE OF INVENTION: A Bacillus Protein Production Cell
FILE REPERENCE: 5861.200-US
CURRENT APPLICATION NUMBER: 60/130,194
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 691.200
PRIOR PILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
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          PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 54, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Sequence 2, Application US/09542749A
// Patent No. 6428981
                                                                                                                              TYPE: PRT
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-28779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bacillus subtilis
US-09-542-749A-2
                                                      NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 28779; LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36,7%
.....hes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: SOYBEAN US-09-247-373B-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER
SOFTWARE: MICL
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Fas
SEQ ID NO 2
LENGTH: 275
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24834

LENGTH: 589
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                          APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 4; Length 578; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                 CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-24834; Sequence 24834; Application US/09252991A; Patent No. 6551795
Sequence 23906, Application US/09252991A
Patent No. 6551795
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US-09-252-991A-23906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 29.2%;
Local Similarity 84.6%;
les 11; Conservative
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                                                              GENERAL INFORMATION: APPLICANT: MArc J.
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LENGTH: 578
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27.5%; Score 49; DB 4; Length 524;
Best Local Similarity 30.0%; Pred. No. 73;
Matches 9; Conservative 8; Mismatches 13; Indels
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Fatent No. 6455672
GENERAL INFORMATION:
APPLICANT: Benfey et al.
TITLE OF INVENTION: Thereof;
FILE REFERENCE: 5914-074-999
CURRENT APPLICATION NUMBER: US/09/186,188B
CURRENT FILING DATE: 1998-11-05
FRIOR APPLICATION NUMBER: 08/42,445
FRIOR FILING DATE: 1997-04-24
FRIOR APPLICATION NUMBER: 08/638,617
                                                                                                                                                      Sequence 56, Application US/08842445A

Patent No. 6441270

SERENTAL INFORMATION:

APPLICANT: Benfey et al.

TITLE OF INVENTION: Thereof

TITLE REFERENCE: 5914-056-999

CURRENT APPLICATION NUMBER: US/08/842,445A

CURRENT PILING DATE: 1997-04-24

SEALLIER RPLING DATE: 1996-04-26

NUMBER OF SEQ ID NOS: 79

NUMBER OF SEQ ID NOS: 79
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                                             6 QNRVHESENMLNSLRELEKQLLDDDDESGG 95
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                       5 QEQLEHRERSLQTLRDIQRMLFPDEKEFTG 34
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NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 524
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OTHER INFORMATION: Xaa - Any Amino Acid
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Best Local Similarity 30.00
Loc 9, Conservative
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ORGANISM: Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Plant
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US-09-186-18BB-56
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Benfey, Philip
APPLICANT: Benfey, Philip
APPLICANT: Dilaurenzio, Laura
APPLICANT: Wiscoka-Diller, Joanna
APPLICANT: Malamy, Jocelyn E.
APPLICANT: Helariutta, Trio
TILLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
FILE REPERENCE: 5914-075-999
CURRENT APPLICANT NUMBER: US/09/186,276B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.1%; Score 50; DB 4; Length 1201; Best Local Similarity 39.1%; Pred. No. 1.3e+02; Matches 9; Conservative 8; Mismatches 6; Indels
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                       10; Indels
                                                                                                                                                                                                                                                                                        37.0%; Pred. No. 26; tive 7; Mismatches
                                                                                      :|: |: :| ||::| || :| || 91 ELQGRKAGMQFLRNMQESLFVSKKNIT 117
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PRIOR FILING DATE: 1997-04-24
PRIOR PEPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSEQ for Windows Version 3.0
                                                            7 QLEHRERSLOTLRDIQRMLFPDEKEFT 33
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OTHER INFORMATION: Xaa = Any Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Matches 9; Conservative
    Best Local Similarity 37.0 Matches 10; Conservative
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October 15, 2003, 10:32:06; Search time 14.8444 Seconds (without alignments) 379.908 Million cell updates/sec
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                        Compugen Ltd.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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                                                                                                                                                                                                                                                                                                                                                                                               600653 seqs, 161128416 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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14: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Sequence 5, Appli	Sequence 15, Appl	Sequence 17, Appl	Sequence 4, Appli	Sequence 3511, Ap	Sequence 8511, Ap	Sequence 12, Appl	Sequence 32, Appl	Sequence 21, Appl	Sequence 30, Appl	Sequence 31, Appl	Sequence 14, Appl	Sequence 16, Appl	Sequence 19, Appl	Sequence 18, Appl
SUMMARIES		er.		US-10-322-579-5	US-10-322-579-15	US-10-322-579-17	US-10-322-579-4	US-10-128-714-3511	US-10-128-714-8511	US-10-053-248-12	US-10-284-753-32	US-10-097-340-21	US-10-284-753-30	US-10-284-753-31	US-10-097-340-14	US-10-097-340-16	US-10-097-340-19	US-10-097-340-18
				15	15	15	15	15	15	12	16	15	16	16	15	15	15	15
		Query Match Length DB		35	1426	1115	35	603	618	294	333	390	433	433	464	643	718	751
	ф	Query	1	100.0	100.0	60.1	37,1	32.3	32.3	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9
		Score	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	178	178	107	99	57.5	57.5	55	55	55	55	55	55	52	55	52
		Result No.		ત	N	ж	4	5	Ø	7	8	60	10	11	12	13	14	15

Sequence 4987, Ap	Sequence 10651, A	Sequence 466, App	Sequence 466, App	4366,	Sequence 11828, A		Sequence 28, Appl		Sequence 323, App		56,	306,	86, A	8,	29	277,	Sequence 15, Appl	Sequence 14821, A	Sequence 11081, A	Sequence 10420, A	Sequence 63, Appl	Sequence 3, Appli		Sequence 3235, Ap	Sequence 5, Appli		Sequence 14264, A	Sequence 12, Appl	2510
9 US-09-815-242-4987	9 US-09-815-242-10651		12 US-09-876-997-466		⊃		12 US-10-236-055A-28			15 US-10-234-432-24							9 US-09-916-790-15	15 US-10-156-761-14821	9 US-09-815-242-11081	15 US-10-156-761-10420	11 US-09-298-523B-63	11 US-09-298-523B-3	15 US-10-128-714-8235	15 US-10-128-714-3235	11 US-09-819-104A-5	9 US-09-867-550-2062	15 US-10-156-761-14264	14 US-10-062-254-12	9 US-09-864-761-42510
434	448	200	200	444	1162	464	804	2654	201	461	524	535	893	1413	2000	868	170	182	198	529	670	711	810	811	2462	100	118	139	142
28.7	28.7	28.7	28.7	28.1	28.1	27.8	27.8	27.8	27.5	27.5	27.5	27.5	27.5	27.5	27.5	27.2	27.0	27.0	26.7	26.4	26.4	26.4	26.4	26.4	26.4	26.1	25.8	25.8	25.8
51	51	21	51	20	20	49.5	49.5	49.5	49	49	49	49	49	49	49	48.5	48	48	47.5	47	47	47	47	47	47	46.5	46	46	46
16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 US-10-322-579-5

```
Sequence 5, Application US/10322579

Publication No. US20030114413A1

SERBERAL INFORMATION:

MAPPLICANT: BASIER, Kortad

APPLICANT: BASIER, Enich

APPLICANT: RENESCH, Barbara

APPLICANT: FROESCH, Barbara

APPLICANT: RENESCH, Barbara

APPLICANT: BUNNES: Lich

APPLICANT: BUNNES: Lich

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON

FILE REFERENCE: Q60361

CURRENT FILING DATE: 2002-12-19

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2001-07-27

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEC ID NOS: 22

SOFTWARE: PATENT ON WIMBER: 60/221, 502

NUMBER OF SEC ID NOS: 22

SOFTWARE: PATENT ON S
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RESULT 2 US-10-322-579-15

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APPLICANT: INTERNALL:
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Ememieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PILING DATE: 2001-04-05
PRIOR PELING DATE: 2001-06-05
PRIOR PELING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
                                                                             APPLICANT: BRONNER, EIICH
APPLICANT: FROESCH, BALTBARA
APPLICANT: FROESCH, BALTBARA
APPLICANT: RAMPS, Thomas
APPLICANT: RAMPS, Thomas
APPLICANT: REAMPS, Thomas
APPLICANT: PETER, Oliver
TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATH
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE REFERENCE: 060361
CURRENT APPLICATION NUMBER: US/09/915,543
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
SOFWHARE: PATENTIN UNDER: 06/221,502
NUMBER OF SEQ ID NOS: 22
SOFWHARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.1%; Score 66; DB 15; Length 35; 31.4%; Pred. No. 0.05;
tive 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |: :| :||| | :: :: |||: : ||
1 ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3511, Application US/10128714; Publication No. US20030119013A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Aspergillus fumigatus
Publication No. US20030114413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.3%
Best Local Similarity 31.4%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Drosophila lgs
US-10-322-579-4
                                                           APPLICANT: BASLER, Konrad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-128-714-3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-128-714-3511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Publication No. US20030114413A1

GENERAL INFORMATION:

APPLICANT: BRUNNER, Erich

APPLICANT: BRUNNER, Erich

APPLICANT: FROESCH, BAT-Dara

TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY

TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY

TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY

TITLE OF INVENTION UNDRER: US/10/322,579

CURRENT FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/221,502

PRIOR APPLICATION NUMBER: 60/221,502

PRIOR APPLICATION NUMBER: 60/221,502
                                                                             APPLICANT: BASLER, Konrad
APPLICANT: BRUNNER ETICH
APPLICANT: BRUNNER ETICH
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Barbara
APPLICANT: FROESCH, Thomas
APPLICANT: FRAMPS, Thomas
APPLICANT: FETER, Oliver
TITLE OF INVENTION: ESERWILL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
FILE REFERENCE: Q60361
CURRENT APPLICATION NUMBER: US/10/322,579
CURRENT APPLICATION NUMBER: US/09/915,543
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,502
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 178; DB 15; Best Local Similarity 100.0%; Pred. No. 3.2e-15; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 383
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Sequence 15, Application US/10322579
Publication No. US20030114413A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human 1gs/bc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NOS: 22
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US-10-322-579-17
                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 15
LENGTH: 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-322-579-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-322-579-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030129655A1 g6572185
US-10-284-753-32
                                          Sequence 32, Application US/10284753

Suguence 32, Application US/10284753

Publication No. UG20030129655A1

GENERAL INFORMATION:
APPLICANT: Klinger, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Wow, Henry
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
FILE REPERENCE: PC-0010-1 CIP
CURRENT PILING DATE: 2000-10-29
FRIOR APPLICATION NUMBER: 09/507,765
PRIOR FILING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGRAM
SEQ ID NO 32
LENGTH: 333
LENGTH: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR PAPLICATION NUMBER: 60/256,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/274,967
PRIOR FILING DATE: 2001-03-14
PRIOR PLILNG DATE: 2001-03-14
PRIOR PLILNG DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR PLILNG DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/315,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GLRTEGLFRRSASVQTVREIQRL 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/10097340; Publication No. US20030087250A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOHN MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMTYAR
APPLICANT: Steve G. KOVATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosemarie SCHMANDT
Xumei ZHAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 52.2%
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ami SEN
                     RESULT 8
US-10-284-753-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                          APPLICANT: Hu, Wengi
APPLICANT: Hishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Ecoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US 60/285,697
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FUBLICATION NO. US20030144188A1
GENERAL INFORMATION:
APPLICAMY: Lin, Biaoyang
TITLE OF INVENTION: Androgen Regulated Nucleic Acid
TITLE OF INVENTION: Molecules and Encoded Proteins
FILE REPERENCE: P-IS 4814
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
45 DGVETEKIREKD --- EVEKKLERMLFGDDEGFVGA 76
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PRIOR FILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8663
SOCTWARE: Patentin version 3.1
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                                                                                         US-10-128-714-8511; Sequence 8511, Application US/10128714; Publication No. US20030119013A1; GENERAL INFORMATION:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-8511
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Best Local Similarity 52.2%
Matches 12; Conservative
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LENGTH: 294
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                                                                                                                                                                                                                                                 Query Match
30.9%; Score 55; DB 15; Length 390;
Best Local Similarity 52.2%; Pred. No. 23;
Matches 12; Conservative 4; Mismatches 7; Indels
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US-10-284-753-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Klinger, Tod M.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Yue, Henry
APPLICANT: Baughn, Mariah R.
TILE OF INVENTION: GTPASE ACTIVATING PROTEINS
FILE REFERENCE: PC-0010-1 CIP
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CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/507,765
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGram
                                                              NUMBER OF SEQ ID NOS: 363
SOFTWARE FRACEO for Windows Version 4.0
SEQ ID NO 21
LENGTH: 390
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                   PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
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Publication No. US20030129655A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-09-26
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US-10-097-340-21
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US-10-284-753-31
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LENGTH: 433
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TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
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                                                                  ; NAME/NET:
; NAME/TET: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030129655A1 404424.5.pseq
US-10-284-753-31
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                                                                                                                                                                        Length 433;
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                                                                                                                                                                      Query Match 30.9%; Score 55; DB 16; Best Local Similarity 52.2%; Pred. No. 26; Matches 12; Conservative 4; Mismatches 7
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CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT ELLING DATE: 2002-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ FOR WINGOWS VERSION 4.0
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Sebastian HOERSCH
Shubhangi KAMATKAR
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Robert C. BAST, Jr.
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Rachel E. MEYERS
Michael MORRISEY
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Best Local Similarity 52.2%
Matches 12; Conservative
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Karen GLATT
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, IITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
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PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PELICATION NUMBER: 60/325,149
PRIOR PELICATION NUMBER: 60/324,967
PRIOR PELING DATE: 2001-03-14
PRIOR PELING DATE: 2001-09-26
PRIOR PLING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PLING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR PRILOR PLING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                       FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
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APPLICANT: Manjula GANRAVARAU
APPLICANT: Sebastian HOERSCH
APPLICANT: Steve G. KOVATS
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
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Robert C. BAST, Jr.
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Karen GLATT
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Karen GLATT
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LENGTH: 718
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APPLICANT:
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APPLICANT: Robert C. BAST, Jr.
APPLICANT: Raren LU
APPLICANT: Karen LU
APPLICANT: Xumei 2HAO
APPLICANT: Xumei 2HAO
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-09/26
PRIOR FILING DATE: 2001-09/26
PRIOR FILING DATE: 2001-09/26
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PLILING DATE: 2001-09-26
PRIOR PLILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: MRI-0530
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT ELLING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/325,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 19, Application US/10097340; Publication No. US20030087250A1; GENERAL INFORMATION:
                                                                    ; Sequence 16, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
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Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
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Sebastian HOERSCH
Shubhangi KAMATKAR
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Rachel E. MEYERS
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Ami SEN
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ORGANISM: Homo sapiens
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US-10-097-340-19
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                                               10-097-340-16
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PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-08-10

PRIOR PLICATION NUMBER: 60/311,732

PRIOR PLICATION NUMBER: 60/323,580

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 20
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Search completed: October 15, 2003, 10:50:58 Job time : 15.8448 secs

509 GLRTEGLERRSASVQTVREIQRL 531

QY Db

Wed Oct 15 11:40:28 2003

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 15, 2003, 10:27:32 ; Search time 8.30739 Seconds Run on:

(without alignments)
405.170 Million cell updates/sec

178 1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA US-09-915-543-15_COPY_349_383 Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_76:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di				
Result No.	Score	Query Match	° Query Match Length	DB	ID	Description
	- 2	32.0		: 2	AB0551	exonuclease SbcC [
7	٠	31.5		~	S51882	topoisomerase I-re
m	9	31.5		a	T46372	hypothetical prote
4	S	30.9		7	AE2895	transcription regu
'n	S	30.9		7	H97670	hex regulon repres
9		30.9	643	7	B59436	ď
7	5	30.6		N	S14065	
- 00	'n	30.1		~	T03455	ALR protein - huma
0	3	30.1	5262	7	T03454	ALR protein - huma
10	23	29.8		N	B70438	hypothetical prote
11	m	29.8	m	Н	E69957	
12	53	29.8	81	N	S62790	mismatch DNA recog
13	Ŋ	29.5	24	7	B70366	hypothetical prote
14	S	29.5			T24343	hypothetical prote
15					T14802	phytochrome B - so
16	22				B47017	probable transcrip
17			332		AD2541	transcription init
18					D82984	pyruvate dehydroge
19					561174	hypothetical prote
20				~	AH0216	+
21		2	237	~	A49940	alpha
22				~	E91056	alpha
23	51	7		7	A85901	,
24	51			7	D96834	hypothetical prote
25	51	7		7	T18801	hypothetical prote
56	51			Н	GNMVMM	6
27	51	28.7	П	7	G90684	ATP-dependent dsDN
28	51	~		7	C85535	ATP-dependent dsDN
29	51	7	1464	~1	S58984	development protei

endopeptidase Clp conserved hypothet	hypothetical prote	hypothetical prote	CDS protein F9L11.	hypothetical prote	conserved hypothet	hypothetical prote	1-pyrroline-5-carb	troponin T, cardia	hypothetical prote	hypothetical prote	L-lactate dehydrog	glycerol-3-phospha	conserved hypothet	hypothetical prote
AD2441 H69337	H69843	S49771	G86454	S67595	D83454	B36329	AE1124	TPCHTC	S72858	T18860	A84142	E81730	T41236	C90796
00	C3	7	7	7	7	~	~	₩.	~	7	7	~	~	~
835	275	319	518	788	1162	1236	266	302	336	830	310	338	420	537
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28.4	28	38	78	3	5	ñ	~	'n	'n	'n	'n	7	CA	. 4
50.5 28.			50 28			50 2			49.5 2		49 2.	49 2	49 2	49

ALIGNMENTS

RESULT 1 AB0551 exonuclease SbcC [imported] - Salmonella enterica subsp. enterica serovar Typhi (str. exonuclease SbcC [imported] - Salmonella enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002	Churchesidu, Abougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far , S.; Moule, S.; O'Gaora, P. Mature 413, 848-852, 2001	A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s. A;Teference number: AB0502; MUID:21534947; PMID:11677608 A;Accession: AB0551	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Cross references: GB:AL513382; PIDN:CAD08850.1; PID:916501663; GSPDB:GN00176 C;Genetics: A;Gene: STY0429 C;Superfamily: sbcC protein	rv Match 32.0%: Score 57: DB 2: Length 1034:
RESULT 1 AB0551 exonuclease Sk C; Species: Sal A; Note: this s C; Date: 09-Not	C; Accession: R; Parkhill, J. th, T.; Conner , S.; Moule, S	A; Authors: Par A; Title: Comp. A; Reference nu A; Accession: A	A;Status: prelir A;Molecule type A;Roos-referent C;Genetics: A;Gene: STY0429 C;Superfamily:	Ouerv Match

Gaps ; Indels 10; Pred. No. 26; 6; Mismatches Best Local Similarity 42.9%; Matches 12; Conservative (

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3 LSQEQLEHRERSLQTLRDIQRMLFPDEK 30 ğ

|: |||: | ||| | |:: | |:: 213 LADEQLQQLEASLQALTDEEKRLLADQQ 240

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topoisomerase I-related protein TRF4 - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein HRF384; protein 00716; protein YOL115w
S.Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000
C;Accession: S51882; S59158; S58774; S66811
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV inclusing a Delta.

A; Reference number: S51848

A;Accession: S51882
A;Accession: S51882
A;Accule type: DNA
A;Residues: 1-584 - VANA
A;Residues: 1-584 - VANA
A;Residues: D:584 - VANA
A;Cross-references: EMBL:248149; NID:9663234; PID:9663237
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A;Fitle: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including a delta element.

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P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan
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A;Accession: H97670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
                                                                                        ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Recession: AE2895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hex regulon repressor [imported] - Agrobacterium tumefaciens (strain C58, Cereon) (Species: Agrobacterium tumefaciens (5.5pecies: Agrobacterium tumefaciens (5.5pecies: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 (5.Accession: H97670
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                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-287 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43579.1; PID:g17741095; GSPDB:GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE007869; PIDN: AAK88321.1; PID: 915157797; GSPDB: GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tho GTPase activating protein RhoGAP8 - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 23-Sep-2002 C; Accession: B59436 By RE: Huckle, E.J. Bsubmitted to GenBank, April 2000 A; Reference number: B59436 A; Accession: B59436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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28;
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 55; 40.0%; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain C58 (Dupont) C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Map position: circular chromosome
C; Superfamily: hypothetical protein ybbH
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: circular chromosome
C; Superfamily: hypothetical protein ybbH
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.9%;
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12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <KUR>
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A; Residues: 1-643 <GOW>
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                                                                                                                                                                                                                       A; Status: preliminary
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                                          A:Status: nucleic acid sequence not shown; translation not shown
A:Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence was submitted to the EMBL Data Library, January 1995
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
A;Title: Isolation of mutants of Saccharomyces cerevisiae requiring DNA topoisomerase I.
A;Reference number: S58774; MUID:96109595; PMID:8647385
A;Reference number: S58774
A;Molecule type: DNA
A;Residues: 1-584 <SAD>
A;Residues: 1-584 <SAD>
A;Residues: 1-584 <SAD>
A;Recence number: S66791
A;Molecule type: DNA
A;Recence number: S66791
A;Molecule type: DNA
A;Recence number: S66791
A;Molecule type: DNA
A;Residues: 1-584 <DNA
A;Residues: 1-584 <D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription regulator, RpiR family Atu2598 [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE2895
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C;Species: Homo sapiens (man)
C;Accession: T46372
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223031
A;Accession: T46372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-859 cAAA>
A;Cross-references: EWBL:AL137528
A;Cross-references: EWBL:AL137528
A;Experimental source: adult testis; clone DKFZp434P1818
C;Genetics:
A;Note: DKFZp434P1818.1
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A; Reference number: S59156; MUID: 96076631; PMID: 7502582
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A; Map position: 15L
C; Keywords: nucleus
                                   A; Accession: S59158
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T46372
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Actions: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, Soetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; May, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetc, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska, A.; Sakuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togonoui, A.; Tosato, V.; Vochigut, Winters, P.; Winters, P.; Winters, R.; Yata, K.; Yoshid
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A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E69957
R;Kunst, F:, Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be.
C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                     R.; Y
                                                                                                                          a novel gene with strong hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ag_1596 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70438
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70438
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C;Accession: T03454
R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human A.R. a novel gene with stron A;Reference number: Z14954; MUID:97388474; PMID:9247308
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A;Residues: 1-5262 <PRA>
A;Cross-references: EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2358285
C;Genetics:
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Pred. No. 4.5e+02;
i; Mismatches 12;
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Pred. No. 16;
7; Mismatches
                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: human ALR protein
C;Keywords: alternative splicing
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Best Local Similarity 42.5%
Matches 17; Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                               SH4065
phytochrome B - rice
C;Species: Organ sativa (rice)
C;Accession: S14065
R;Debesh, K.; Tepperman, J.; Christensen, A.H.; Quail, P.H.
Mol. Gen. Genet. 225, 305-313, 1991
A;Title: phyB is evolutionarily conserved and constitutively expressed in rice seedling
A;Reference number: S14065; MUID:91172131; PMID:2005872
A;Actuas: prelliminary
A;Molecule type: DNA
A;Residues: 1-1171 CDEH>
A;Cross-references: GB:X57563; NID:96469490; PIDN:CAA40795.2; PID:96469491
C;Genetics:
A;Genetics:
A;Genetics: A;Genetics: A;Genetics: Phytochrome homology
C;Keywords: chromoprotein; phytochrome homology
C;Keywords: chromoprotein; phytochrome homology <br/>C;Keywords: chromoprotein; phytochromely (cys) (covalent) **status predicted
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C:Date: 24-Mar-1997
C:Sate: 24
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C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
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Pred. No. 4.3e+02;
4; Mismatches 12; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1171;
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                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GLSQEQLEHRERSLQTLRD----IQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54.5; DE Pred. No. 63; 4; Mismatches
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LSQEQLEHRERSLQTLRDIQRMLFPDE 29
                                                                                                                                  2 GLSQEQLEHRERSLQTLRDIQRM 24
                   4,
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Best Local Similarity 42.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 48.1
                   Conservative
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                   12;
                   Matches
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Score 53; Pred. No.

29.8%; 52.6%;

Q δ

27 4.

9 EHRERSLQTLRDIQRMLFP

Conservative

Local Similarity les 10; Conserv

Query Match Matches

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phytochrome B - sorghum (fragment)
C;Species: Sorghum bloolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14802
E;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mull)
submitted to the EMBL Data Library, April 1996
A;Description: The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phyto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Map position: 5
A:Introns: 22/2, 88/2; 117/3; 185/1; 221/3; 280/3; 349/2; 427/2; 532/2; 637/1
C;Superfamily: cholinesterase; cholinesterase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: 281112; PIDN: CAB03272.1; GSPDB: GN00023; CESP: T02B5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000 C;Accession: T24343 R;McMurray, A. Submitted to the EMBL Data Library, October 1996 A;Reference number: 219878 A;Reference number: 219878
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5:
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                                                                                 Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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A; Experimental source: cultivar 58M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intron positions not resolved (incomplete sequence)
           C; Superfamily: Aquifex aeolicus hypothetical protein aq_755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: phytochrome; phytochrome homology c; Reywords: chromoprotein; photoreceptor; phytochromobilin F; 233/Binding site: phytochromobilin (Cys) (covalent) *stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 LSEEQVENTYSCLRKKSAQQILDAQLWLLQNSTYFLGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LSQEQLEH----RERSLQTLRDIQRMLFPDEKEFTGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T02B5.1 - Caenorhabditis elegans
                                                                                     ;;
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Pred. No. 1e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                         ; Score 52.5; Di
; Pred. No. 20;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSQEQLEHRERSLQTLRDIQRMLFPDE 29
                                                                                                                                                                                                                                    10 HRERSLQT-LRDIQRMLFPDEKEF 32
                                                                                                                                                                                                                                                                              |: ||: :|:|:| |||| | HKTSLRKFVREIEKMVFEAEKEF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: clone T02B5
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Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Caenorhabditis elegans
                                                                             Query Match 29.5%;
Best Local Similarity 45.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z18185
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Best Local Similarity
Matches 14; Conserv
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A; Residues: 1-705 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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C.Species: Thermus aquaticus
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C.Accession: 862790
C.Racession: 862790
Mulleic Acids Res. 24, 640-647, 1996
A;Title: Mismatch DNA recognition protein from an extremely thermophilic bacterium, Ther A;Reference number: 862790; MulD:96177563; PMID:8604304
A;Reference number: 862790; MulD:96177563; PMID:8604304
A;Reference number: 862790
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-818 
A;Residues: 1-818 
A;Ross-references: EMBL:D63810
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By 1036 A) Protein ad 755 - Aquifex aeolicus (5.5pecites: Aquifex aeolicus C.5pecites: Aquifex aeolicus (5.5pecites: Aquifex aeolicus (5.5pecites: Aquifex aeolicus (5.5pecites: Aquifex aeolicus (5.5pecites: Arg. 1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000 (5.5Accession: B70366 R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ow Nature 392, 353-358, 1998 A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A; Reference number: A70300; MUID:98196666; PMID:9537320 A; Accession: B70366 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-242 < AQFE? AA, ACCESION A; ACCESION A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000706; NID:92983327; PIDN:AAC06923.1; PID:92983334; GB:AE00065 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: muts
C; Function:
C; Function:
A; Description: implicated in DNA mismatch repair; binds to DNA and specifically recogniz
atched DNA [validated, MUID:96177563]
C; Superfamily: DNA mismatch repair protein muts
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69957
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-376 cKUN>
A;Experimental source: strain 168
A;Experimental source: strain 168
C;Genetios:
A;Gene: yqqT
C;Superfamily: endopeptidase I
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Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
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ed. No. 28;
Mismatches 5
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465

ò q A; Gene: aq_755

6 EQLEHRERSLOTLRDIQRMLFPDEKE 31

Query Match 29.8%; Best Local Similarity 42.3%; Matches 11; Conservative

ä

1;

Search completed: October 15, 2003, 10:33:10 Job time : 11.3074 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

2003, 10:27:32 ; Search time 4.22179 Seconds October 15, Run on:

(without alignments)
389.867 Million cell updates/sec

US-09-915-543-15_COPY_349_383 178 1 DGISQEQLEHRERSLQTLRDIORMLFPDEKEFTGA 35 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched: 127863 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	000512 homo sapien	drosc					_	bacillus	thermus	056239 thermus the		fusobact	aduifex		Q03065 anabaena sp			P37328 escherichia		Q9cxp4 mus musculu							arap	Q01970 homo sapien		4	0	0608 rattu	0
SUMMARIES	ID	BCL9_HUMAN	BCL9_DROME	TRF4_YEAST	HEM1_SYNEL	RHG8_HUMAN	ASH3_MOUSE	PHYB_ORYSA	YQGT_BACSU	MUTS_THECA	MUTS_THETH	ASH3_HUMAN	RRF_FUSNN	Y755_AQUAE	PHYB_SORBI	RPSB_ANASP	MUTS_THEAQ	RGA2_YEAST	YFHG_ECOLI	POL_MMTVB	RHG8_MOUSE	MOZ_HUMAN	TRT2_CHICK	DYN1_CAEEL	LDH_BACHD	PLSX_STAAW	YDBJ_SCHPO	DML1_ARATH	PIP3_HUMAN	YWKC_BACSU	CARB_METMA	PHYB_TOBAC		T2D1_HUMAN
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	Length																																1505	
	% Query Match	100.0	37.1	31.5	30.9	30.9	30.6	30.6	29.8	29.8	29.8	29.5	29.2	29.2	29.2	29.5	29.5	29.5	28.7	28.7	28.1	28.1	27.8	27.8	27.5	27.5	27.5	27.5	27.5	27.2	27.2	27.2	27.2	71.7
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	Result No.		71	m	4	5	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

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099un9 staphylococ P34934 sus scrofa P47040 saccharomyc 08032 saccharomyc P41439 enterococcu 002849 ovita aries QBtvb2 methanopyru P5059 saccharomyc P44834 haemophilus QBra24 thermoanaer P56790 agrobacteri Q9f984 bacillus st
PLSX_STAAM HS7X_PIG HS7X_PIG CQ45_YEAST CQ45_YEAST NTPI_ENTHR PD13_SHEEP PYRB_MSTRA MNT2_YEAST MOT2_YEAST MT2_HAEIN RRF_THETN HIS4_AGRT5 HS10_BACST
наннананна
328 3328 408 650 664 558 309 184 247 247
27.0 27.0 27.0 27.0 27.0 26.7 26.7 26.7 44.9
44444 7.74 75 44448 75 7.447
80000000444444444444444444444444444444

ALIGNMENTS

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Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.; Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K.; Nellen B., Signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex."; cell 109:47-60(2002).
-1- FUNCTION: Involved in signal transduction through the wnt pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: It is uncertain whether Met-1 or Met-27 is the initiator. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 1391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: Involved in a t(1,14)(q21,q32) chromosomal translocation found in a patient with precusor B-cell acute lymphoblastic leukemia (ALL). This translocation leaves the coding region intact, but may have pathogenic effects due to alterations in the expression level of BCL9. Several cases of translocations within the 3' untranslated region of BCL9 have been found in B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBGNIT: Binds to beta-catenin (CTNNB1), PYGOI and PYGO2.
-i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- TISSUE SPECIFICITY: Detected at low levels in thymus, prostate, testis, ovary and small intestine, and at lower levels in spleen, colon and blood.
                                                                                                                                                                                                                                                                                                                                                                        Distriction of translocation t(1;14)(q21;q32) defines a novel gene (BCL9) at chromosome 1q21."; Blood 91:1873-1881(1998).
                                                                                                                                                                                                                                                                                    TISSUE-Fetal brain;
MEDILE-98158621; PubMed-9490669;
MILLIS T.G., Zalcberg I.R., Colgnet L.J.A., Wlodarska I., Stul M.,
Jadayel D.M., Bastard C., Treleaven J.G., Catovsky D., Silva M.L.M.,
                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                       28-FEB-2003 (Rel. 41, Created)
8-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
8-cell lymphoma 9 protein (Bcl-9) (Legless homolog).
                                   1426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21952490; PubMed=11955446;
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                   STANDARD;
                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          maliquancies.
                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                             Dyer M.J.S.;
                                   BCL9_HUMAN
000512;
                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
FUNCTION.
                   BCL9_HUMAN
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RESULT 1
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SEQUENCE
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RADDIANELSUJSOUGH, PURDACE-10/31124,

RADDIANELSUJSOUGH, PURDACE-10/31124,

RADDIANELSUS S. B., Holt R.A., Galle R.F.,

RADDIANELS R.A., Lewis S.E., Richards S.A. Sabhurner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RADDIANELS R.A., Dayle C., Baxerdale J., Bayraktaroglu E., Basaley E.M.,

RADII J.F., Agbayani A., An H.J., Andrews-Prennkoch C., Baldwin D.,

RADII J.F., Dayle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RADIN R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,

RADORON R.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RADDIANELS B., Marnel A.E., Garg N.S., Gelbart W.M., Glasser R.,

RADDIANELS B., Marnel A.E., Garg N.S., Gelbart W.M., Glasser R.,

RADDIANELS B., Marnel T.J., Helman T.J., Hernandez J.R., Houck J.,

RADDIANELS B., Marnels B., Marne
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota,
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                          Length 1426;
                                                                                              Nuclear protein; Chromosomal translocation; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                 MW; A240A487716B7F1B CRC64;
                                                                                                                                                                                                                                                                                                                          100.0%; Score 178; DB 1;
100.0%; Pred. No. 3.1e-15;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL9_DROME STANDARD; PRT; 1469 AA. 0961D9; 094VD2; 1. Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) BCL9 DMMOLOG (Legless protein).
                                                                                                                                                               CINNB1-BINDING.
                                                                                                                                                                                     POLY-PRO 1.
POLY-PRO 2.
                                                                                                                                                                                                                                   POLY-ALA.
POLY-PRO 3.
                                                                                                                                            PRO-RICH
EMBL; Y13620; CAA73942.1; ALT_FRAME
Genew; HGNC:1008; BCL9.
                                                MIM; 602597; -.
GO; GO:0007048; P:oncogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                              149314
                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.
Matches 35; Conservative
                                                                                                               Wnt signaling pathway.
                                                                                                                                                                                                                                                                                 1426 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                               347
331
514
900
970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                    DOMAIN
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BEL9_DROME
ID DATO 28-FEBB
DT 15-SEP
GN BEL19
GN BEL19
GN BEL19
GN BEL19
GN BEL19
GN BEL10
GN BEL1
                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005634; C:nucleus; IEP.
GO; GO:0030528; F:transcription regulator activity; IPI.
GO; GO:003177; P:positive regulation of Wnt receptor signali. . .; IPI.
GO; GO:0007367; P:seqment polarity determination; IMP.
Nuclear protein; Developmental protein; Segmentation polarity protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L->F: IN ALLELE LGS-17E; SEGMENT POLARITY
                                                                                                                                                                                                                                         STRAIN=Berkeley; TISSUE=Embryo;
MEDILINE=22426066; PubMed=12537569;
Stapleton M., Carlon J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A prosophila full-length CDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21952490; PubMed-11955446;
Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S.,
Murone M., Zuellig S., Basler K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- FUNCTION: Involved in signal transduction through the wnt pathway.
-1- SUBGNIT: Binds to ARM and PYGO.
-1- SUBCELLUIAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Wnt/wingless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex."; Cell 109:47-60(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 6-1469 FROM N.A., AND MUTAGENESIS OF GLY-514; LEU-534 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I->K: IN ALLELE LGS-17P.
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASN-RICH.
GLN-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1469 AA; 153759 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1449
1169
514
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les 11; Conserv
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signaling paraling paralling paralling paralling sign
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P53632;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARHGAP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHG8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                    uerica erumini.
Yeast 11:1069-1075(1995).
-!- FUNCTION: ESSEWITAL PROTEIN REQUIRED FOR PROPER NUCLEAR DIVISION
IN MITOSIS. MAY MEDIATE MITOTIC CHROWSOME CONDENSATION.
-!- SIMILARITY: BELONGS TO THE CIDI/TRF4/TRF5 FAMILY.
                                                                                                                                                                                                                                                        Vandenbol M., Durand P., Portetelle D., Hilger F.; "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the Tyl-H3 retrotransposon, the sufl(+) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and a
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-96109595; PubMed-8647385;
Sadoff B.U., Heath-Pagliuso S., Castano I.B., Zhu Y., Kieff F.S.,
Christman M.F.;
                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                             "Isolation of mutants of Saccharomyces cerevisiae requiring DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGD; S0005475; TRF4.
GO: 600005534; C:nucleus; IDA.
GO: 600003887; F:DA-directed DNA polymerase activity; IDA.
GO: GO:0006265; P:DNA topological change; IGI.
GO: GO:0007076; P:mictic chromosome condensation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.5%; Score 56; DB 1; Length 584; 36.0%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66030 MW; 8A58B29E4BFDC022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamyl-tRNA reductase (EC 1.2.1.-) (GluTR).
HEMA OR TLL1738.
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 SREEIEIRNQIISTIREAVKQLWPD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SQEQLEHRERSLQTLRDIQRMLFPD 28
                                      Topoisomerase 1-related protein TRF4. TRF4 OR YOL115W OR 00716 OR HRC584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002934; NTP_transf.
Interpro; IPR001201; PPB-25A_core.
Interpro; IPR02058; PAP_assoc.
Pfam; PF01909; NTP_transf_2; 1.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-96076631; PubMed=7502582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-SEP-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U31355; AAC49091.1; -. EBML; Z48149; CAA88145.1; -. EMBL; Z7857; CAA99134.1; -. PIK; S51882; S51882.
                                                                                                                                                                                                         Genetics 141:465-479(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF03828; PAP_assoc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 9; Conserv
                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                              topoisomerase
                                                                                                                                                                                                                                                                                                            delta element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEM1_SYNEL
Q8D153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                          Semialdehyde + NADP(+) + tRNA(Glu).
--- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.
Involved in chlorophyll biosynthesis.
--- SIMILARITY: Belongs to the glutamyl-tRNA reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00745; GlutR_dimer; 1.
Pfam; PF05201; GlutR_N; 1.
TIGRAM; TIGROINS; hemax; 1.
PROSTIE; PS00747; GLUTR; FALSE_NEG.
POTPHYRIN blosynthesis; Chlorophyll blosynthesis; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 4).

Gu J.R., Wan D.F., Zhao X.T., Zhao X.M., Jiang H.Q., Zhang P.P.,
Gu J.R., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
Yu J., Han L.H.;
"Novel human cDNA clone with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHG8_HUMAN STANDARD; PRT; 718 AA.
Q9NSG0; 075983; 095695; Q96RW1; Q96RW2; Q9HA49; Q9HC46; Q9NVX8;
Q9NXL1; Q9UH20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE (BY SIMILARITY).
D84CE5A1D2AA777E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rho-GTPase-activating protein 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 1
Pred. No. 8.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00087; -; 1.
InterPro; IPR000343; GlutR.
InterPro; IPR000594; Thif_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SORDLESRORAMOTLODL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SQEQLEHRERSLQTLRDI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP005375; BAC09290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 AA; 47596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADP; Complete proteome.
ACT_SITE 50 50
                                                                                                               FROM N.A.
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detected are isoforms 1 to 7. Experimental confirmation may be

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RP SEQUENCE FROM N.A.

RA DUAINE-20057165; Dubbed-10591208;

RA DUAINE-20057165; Dubbed-10591208;

RA DUAINE-20057165; Dubbed-10591208;

RA DUAINE I., HUNT A.R., COILING J.E., BIRGES K.N., BEASER O.P.,

RA BAGGILE, BAIREY S.E., Falidgemen A.M., Buck D., Burgess J.,

BIT C.P., Blakey S.E., Falidgemen A.M., Buck D., Burgess J.,

BUTTIL W.D., BUTTON J., Carder C., Calter N.P., Chen Y., Clark G.,

RA Cledg S.M., Cobley V.E., Collier R.E., Connor R.,

RA CLEGG S.M., Cobley V.E., Collier R.E., Connor R.,

RA CLEGG S.M., Flending K., French L., Garner A.A.,

Glibert J.G.R., Goward M.E., Grafham D.V., Girffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcort R.W., Durbin R.M., Ellington A.G.,

RA Hall R.E., Hall-Tamlyn G., Heathcort R.W., Mine S.A., Morthnore B.J.C.T.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Iloyd D.M.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Iloyd D.M.,

RA Martyn I.D., Mashrenghi-Wolmamadi M., Matthews L.H., Mccann O.T.,

RA Abrillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Milliams L., Williams S.A., Williamson H., Wilmer T.E., Williams S., Wawasaki K., Sasaki T., Aacki W., Miles Y., Shimizu N.,

RA Mincshima S., Kawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Kawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Kawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Wawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Wawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Wawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Wawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mincshima S., Wawasaki K., Sasaki T., Aacki W., Mitzuyama S.,

RA Mang Q., Wang Y., Wang Z., White J., Willingham D., Willing T.,

RA Kang Q., Wang X., Milliams D., Williams D., Solon D., Solon D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: GTPase activator for the Rho-type GTPases by converting
them to an inactive GDP-bound state (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim U.J., Shizuya H., Simon M.Ĭ., Dumanski J.P., Peyrard M., Kedra D. Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.;
                                                                                                                                                                                             TISSUB-Colom nucosa, and Mammary gland;
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MCD6Tmid H.E., Hu S., Grundy P., Trichet V.;
"ARHGAP8: a putative tumor-suppressor gene on chromosome 22q13.3.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA sequence of human chromosome 22."; nature 402:489-495(1999).
                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 5; 6 AND 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 3).
Goward M.E., Huckle E.J.;
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Comment=Additional isoforms seem to exist. Full isoforms so far

Event=Alternative splicing; Named isoforms=8;

ALTERNATIVE PRODUCTS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRRSRSGDVLAKNPVVRSKSYNTPLLNPVQEHEAEGAAAGG
STRRHSVSRPARSPEGGESDPPEGGEPTRSSPAPHSG
PCPRELXPTTQPPEGGLDPRSSLPRSSPENLVDQILESVD
SDSEGIFIDFGRGSGMSDLEGSGGRQSVV (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LORDKAAAAAVLGAVRKRPSVVPMAGQDPALSTSHPFYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHGILQVAGDDRFGRRVVTFSCCRMPPSHELDHQRLLEYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTLDQYVENDYTIVYFHYGLNSRNKPSLGWLQSAYKEFDRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGDLTMWPRLVSNSKLKRSSHLSLPKYWDYRYKK -> KRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform 1 and isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                             IsoId=09NSG0-3; Sequence=VSP_001645, VSP_001649, VSP_001653, VSP_01655;
                                                                                                                                                                                                                                                                   isoid=Q9NSG0-8; Sequence=VSP_001646, VSP_001648, VSP_001650,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 1 and isoform 2)
                                                                   IsoId=Q9NSG0-2; Sequence=VSP_001645, VSP_001649, VSP_001652;
                                                                                                                                                                                                                         Missing (in isoform 5 and isoform Fride-Wgr -001647.
FRERYE -> MAPMPT (in isoform 7).
FFIIG-VSP_001648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoform 4 and isoform 7).
                                                                                                                                                                    IsoId=Q9NSG0-5; Sequence=VSP_001650, VSP_001654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 7). /FTId=VSP_001646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VSP_001645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VSP_001649
                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 CRAL-TRIO domain. SIMILARITY: Contains 1 Rho-GAP domain.
                                                                                                                                                                                              IsoId=09NSG0-6; Sequence=VSP_001647;
                                                                                                                                         IsoId=Q9NSG0-4; Sequence=VSP_001651;
                                                                                                                                                                                                                                                                                   VSP_001654;
                                      IsoId=Q9NSG0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTPase activation; Alternative splicing. DOMAIN 267 453 CRAL-TRIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRAL-TRIO.
RHO-GAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AK022305; BAB14008.1; EMBL, AL355192; CAB90248.1; EMBL, 298743; CAB11416.1; ALT_INIT. EMBL, 293244; CAB07531.1; ALT_SEQ. EMBL; 283838; CAB62993.1; ALT_INIT.
             lacking for some isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:677; ARHGAPB.
InterPro; IPR001251; CRAL_TRIO.
InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00620; RhoGAP; 1.
SMARY; SM00324; RhoGAP; 1.
PROSITE; PS50194; RAL_TRIO; 1.
PROSITE; PS50238; RHOGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF195968; AAK58136.1; -. AF195969; AAK58137.1; -. AK000192; BAA90999.1; -. AK001306; BAA91614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF177331; AAG17975.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B59436; B59436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1RGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q07960;
                                                                                                                                                                                  Name=5
                                                     Name=1
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SEQUENCE
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"MASH3 a novel basic helix-loop-helix protein that inhibits myogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=214389. PubMed=11528127;
Amid C., Bahr A., Mujica A., Sampson N., Bikar S.E., Winterpacht A., Zabel B., Hankeln T., Schmidt E.R.;
Zabel B., Hankeln T., Schmidt E.R.;
Zabel B., Hankeln T., Schmidt E.R.;
architecture of a conserved syntenic region on human chromosome architecture of a conserved syntenic region on human chromosome [1ppls. 3 (including gene ST5) and mouse chromosome 7.";
[1ppls. 3 (including gene ST5) and mouse chromosome 7.";
[1ppls. 3 (including gene ST5) and mouse chromosome 7.";
[1ppls. 3 (including gene ST5) and mouse chromosome 7.";
[1ppls. 3 (including gene ST5) and mouse chromosome 7.";
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[1ppls. 5 (including gene ST5) and mouse chromosome 7."
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KGPDSQHFSFAGLLLYCNNSAGLCSSKTLWTLKCEFHVIFT
                                                                                                                               YKKNLKALYVVHPTSFIKVLWNILKPLISHKFGKKVIYFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Achaete-scute homolog 3 (bHLH transcriptional regulator Sgn-1) (Mash-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Specifically expressed in the salivary duct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshida S., Ohbo K., Takakura A., Takebayashi H., Okada T., Abe K.,
Nabeshima Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sgn1, a basic helix-loop-helix transcription factor delineates the salivary gland duct cell lineage in mice.";
                                                                                                                                                                                                     CHETFECFFSTT (in isoform 2).
/FTIG-VSP_001653.
Missing (in isoform 4 and isoform 7).
/FTIG-VSP_001654.
Missing (in isoform 2).
                  Missing (in isoform 3).
/FIId=VSP_001651.
Missing (in isoform 1 and isoform 6).
/FIId=VSP_001652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in C2C12 cells.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7181835625487465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_001656
Missing (in isoform 6).
/FTId=VSP_001657.
                                                                                                                                                                                                                                                                                                                                                                  -> A (in isoform 6).
                                                                                                                                                                                                                                                                                                                       /FTId=VSP_001655.
     /FTId=VSP_001650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 GLRTEGLFRRSASVQTVREIQRL 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.
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52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       718 AA; 81953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.9
Best Local Similarity 52.2
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      580
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                                311
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                                VARSPLIC
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                                                                                                                                                                                                                                                                                                                                          EMBL; AB046448; BAB83301.1;

EMBL; A4400878; CAB92296.1;

EMBL; A4400878; CAB92296.1;

EMBL; A4400878; CAB92296.1;

GO; GO:0005634; C:ucucleus; IDA.

GO; GO:000567; C:transcription factor complex; IPI.

GO; GO:000577; F:DNA binding activity; IDA.

GO; GO:000575; F:protein binding activity; IPI.

GO; GO:000575; P:regulation of transcription from Pol II pro. .; IDA.

FFORDIO: HEM! 1.

SMART; SM00353; HLH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. ASC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSTTE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
Transcription regulation; Repressor; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dehesh K., Tepperman J., Christensen A.H., Quail P.H.; "phyB is evolutionarily conserved and constitutively expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20245 MW; D89E56C8A9D3440B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: || | :: || | :: || | 119 LPEDYLEKRLSKVETLRAAIKYISYLQSLLYPDESE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-cv. Indica-IR36; TISSUE-Seedling shoot; MEDLINE-91172131; PubMed-2005872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 22, Last sequence update) (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54.5; D
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.6%; Sco
llarity 36.1%; Pro
Conservative 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last seq
                                                                                                                                                                                                                                                                                                                        EMBL; AJ277605; CAC37689.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 13; Conserv
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28-FEB-2003 (Re-
Phytochrome B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHYB OR PHYB1.
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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STRALM-168 / JH042;
MEDLINE-97124195; Pubbed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                  PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE. SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY. SIMILARITY: CONTAINS 2 PAS (PER-ARMT-SIM) dimerization domains. SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 CHROMOPHORE (BY SIMILARITY).
128384 MW; E8292E88B769BF16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bācillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.
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PAS 2.
HISTIDINE KINASE.
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54.5;
Pred. No. 3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LSQEQLEHRERSLQTLRDIQRMLFPDE 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASe_c; 1.
SMART; SM00388; HisKa; 1.
SMART; SM00091; PAS; 2.
TIGRFAMS; TIGR00229; sensory_box; 2.
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003594; Arpbind_Arpase.
InterPro; IPR003018; GAF.
InterPro; IPR003661; His_KinA.
InterPro; IPR000467; His_Kinase.
InterPro; IPR000014; PAS_domain.
InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00245; PHYTOCHROME_1; 1. PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00512; H1sKA; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50109; HIS_KIN; 1. PROSITE; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                  EMBL; X57563; CAA40795.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.6%;
48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein yggT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1161
                                                                                                                                                                                                                                                                                                       PIR; S14065; S14065.
Gramene; P25764; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQGT_BACSU
P54497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YOGT_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                         RA KUDILINE-94044031; Dubmed-35645/f);

RA KUNST F., Oggaswara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brotriss R., Bourster L., Brans A., Braun M., Briggell S.C., Bron S.,
RECUILLE S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brischi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Funer C., Fullich K.M., Dusterhoft A., Enrlich S.D., Emmerson P.T.,
RA Entiz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haleoh J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kutita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kutita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tanakoshi A., Tanaka T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,
Minters P., Wipat A., Yandenbol M., Vaniner R., Vasacrotti A.,
Wanbutt R., Wandutt R., Wadder E., Wedler H., Weitzenegger T.,
RA Vasi A., Vasikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
Rabertis A., Wandule S., Wandenbol M., Vanner M., Danchin A.;
Rabertis A., Wandule S., Wandenbol M., Vanner M., Danchin A.;
Rabertis A., Wandule S., Wandenbol M., Vanner M., Danchin A.;
Rabertis A., Wandulet S., Wandenbol M., Vanner M., Backer S., Wander S., Wa
Kobayashi Y.; "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
-!- SIMILARITY: STRONG, TO B.SPHAERICUS GAMMA-D-GLUTAMYL-L-DIAMINO ACID ENDOPEPTIDASE I (EC 3.4.99.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 AA; 43439 MW; 1075CDC124823BB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subtilist; BG11687; yqgT.
InterPro; IPR000834; Zn_carbOpept.
Pfam; PR00246; Zn_carbOpept; 1.
PRINTS; PR00765; CRBOXYPTASEA.
SWART; SM00631; Zn_Pept; 1.
                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                          Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; 52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHSGKELQTIQDIKRFLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D84432; BAA12523.1; -. EMBL; Z99116; CAB14414.1; -. PIR; E69957; E69957. MEROPS; M14.008; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                        sporulation genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
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ASH3_HUMAN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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DALLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics in the There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This protein is involved in the repair of mismatches in Now. It is possible that it carries out the mismatch recognition step. This protein has a weak ATPASE activity (By similarity). SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                          Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                     STRAIN-GK24;
Nashiru O., Park B.C., Ko J.H., Kim J.S., Koh S.K., Lee H.C.,
Kim C.H., Lee S.Y., Lee D.-S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.8%; Score 53; DB 1; Length 817; 42.3%; Pred. No. 31; Live 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00533; MUTSU; 1.
TIGREMS; TIGRO170; MUTSI; 1.
PROSITE; PS00486; DNA, MISMATCH_REPAIR_2; 1.
DNA, TEPAIR; ATP-binding; DNA-binding.
NP_BIND 589 596 ATP (POTENTIAL).
NP_BIND 71 NA. 91179 MW; 61EA066FB84BA761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTS_THETH STANDARD; PRT; 818 AA. Q56239; 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
                                         817 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 EQLEHRERSLQTLRDIQRMLFPDEKE 31
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA mismatch repair protein muts
                                                                                                                                                  DNA mismatch repair protein mutS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF007553; AAD01407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00096; -; 1.
INTERPRO; IPR005748; MULS1.
INTERPRO; IPR000432; MULS_C.
INTERPRO; IPR002863; MULS_C.
Pfam; PF01624; MULS_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05188; MutS_II; 1.
Pfam; PF05192; MutS_III; 1.
Pfam; PF05190; MutS_IV; 1.
Pfam; PF00488; MutS_V; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD001263; Muts_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.39
Watches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00534; MUTSac; SMART; SM00533; MUTSd; 1
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus thermophilus.
                                                                                                                                                                                         Thermus caldophilus
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=274;
                                                                                                                                                                                                                                                      NCBI_TaxID=272;
                                                                                  30-MAY-2000
                                                                                                      30-MAY-2000
28-FEB-2003
                                           MUTS_THECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus.
                                                                                                                                                                                                                                       Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTS_THETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTS.
                            MUTS_THECA
                                                                                                                                                                        MUTS.
    RESULT 9
                                             SO THE PART OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCCORDINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                       MutS protein.";
Nucleic Acids Res. 26:4153-4159(1998).
--- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a maximal ATPase activity at 80 degrees
                                                                                                                                                                                                                                         STRAIN=HB8 / ATCC 27634;
MEDLINE-98391738; PubMed-9722634;
Tachiki H., Kato R., Masui R., Hasegawa K., Itakura H., Fukuyama K.,
Kuramitsu S.;
                                                                                                                                                                                                                                                                                                                                                                           Domain organization and functional analysis of Thermus thermophilus
                                                                                                        Takamatsu S., Kato R., Kuramitsu S.;
"Mismatch DNA recognition protein from an extremely thermophilic
bacterium, Thermus thermophilus HB8.";
Nucleic Acids Res. 24:640-647(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9NQ33; Q8WYQ6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Achaete-scute homolog 3 (bHLM transcriptional regulator Sgn-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ceisius. Binds double-stranded DNA.
SUBUNIT: Homotetramer.
SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
[1] SEQUENCE FROM N.A., SEQUENCE OF 1-20, AND CHARACTERIZATION. STRAIN-HBB / ATCC 27634; MEDLINE=96177563; Pubmed=8604304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 1; Length 818;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
657FD676BF033506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A2.
B; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGRO1070; mutS1; 1.
PROSITE: PS00486; DNA_MISMATCH_REPAIR_2;
DNA_EEPAIR; ATP-binding; DNA-binding.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 EQLEHRERSLQTLRDIQRMLFPDEKE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818 C.
597 AT
91249 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00096; -; I.
InterPro; IPR005748; MutS1.
InterPro; IPR000432; MutS_C.
InterPro; IPR002863; MutS_C.
Pfam; PF01624; MutS_II; I.
Pfam; PF05192; MutS_III; I.
Pfam; PF05199; MutS_III; I.
Pfam; PF05190; MutS_III; I.
Pfam; PF06190; MutS_III; I.
Pfam; PF06190; MutS_III; I.
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Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D63810; BAA09880.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00534; MUTSac;
SMART; SM00533; MUTSd; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 2
274 5
570 8
590 5
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1755_AQUAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y755_AQUAE
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                                                                                                                                                                                                                                                                                                                                                                   BHLH protein (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. ASC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                          similarity).
SUBUNIT: Efficient DNA binding requires dimerization with another
                                                                                                                                                                                                                 MEDLINE-21418998; PubMed-11528127;
Amid C., Bahr A., Mujica A., Sampson N., Bikar S.E., Winterpacht A., Zabel B., Hankeln T., Schmidt E.R.;
"Comparative genomic sequencing reveals a strikingly similar architecture of a conserved syntenic region on human chromosome 11p15.3 (including gene ST5) and mouse chromosome 7.";
Cytogenet. Cell Genet. 93:284-290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                               Yoshida S., Ohbo K., Takakura A., Takebayashi H., Okada T., Abe K.,
Nabeshima Y.;
"Sgn1, a basic helix-loop-helix transcription factor delineates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding; Nuclear protein.
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            FUNCTION: Transcriptional repressor. Inhibits myogenesis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.5%; Score 52.5; DB 1; Length 180; 36.1%; Pred. No. 6.6; tive 7; Mismatches 9; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosome recycling factor (Ribosome releasing factor) (RRF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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C9B90C8B5DE94F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPEEYLEKRLSKVETLRAAIKYINYLQSLLYPDKAE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LSQEQLEHRERSLQTLRD-----IQRMLFPDEKE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusobacterium nucleatum (subsp. nucleatum).
                                                                                                                                                              salivary gland duct cell lineage in mice.";
Dev. Biol. 240:517-530(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ400877; CAB92288.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Repressor;
DNA_BIND 95 105 BASIC DO
                                                                                   SEQUENCE FROM N.A. MEDLINE-21643927; PubMed=11784080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew, HGNC:740; ASCL3.
InterPro, IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB046450; BAB83913.1; -.
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180 AA; 20796 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00038; HLH 1; 1. PROSITE; PS50888; HLH 2; 1.
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                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00353; HLH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
ses 13; Conserv
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                         NCBI_TaxID=9606;
ASCL3 OR SGN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRR OR FN1623
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Q8R529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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ID RRF_F
AC Q8R5Z
DT 28-FE
DT 28-FE
DT 28-FE
DT 28-FE
CO RESON
OS Bacte
OC Fusob
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Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Tansen N., Kyrpides N., Overbeek R.;
Tenstein M., Kyrpides N., Overbeek R.;
Tenstein M., Kyrpides N., Overbeek R.;
Tenstein ArcC 25586.
The nucleatum strain ArcC 25586.
The Bacteriol. 184:2005-2018(2002).
The Puncrion: Responsible for the release of ribosomes from messenger RNA at the termination of protein biosynthesis. May increase the efficiency of translation by recycling ribosomes from one round of translation to another (By similarity).
The SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
The SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.5%; Score 52.5; DB 1; Length 190; 36.1%; Pred. No. 7;
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NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81BD4A7A293B2814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 ISEDELKKEETNVQTLTDKYVKEIDDLLAKKEKEIT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LSQEQLEHRERSLQTLRD----IQRMLFPDEKEFT 33
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD004103; ŘRF; 1.
TIGRRAMS; TIGR00496; frr; 1.
Protein biosynthesis; Complete proteome.
SEQUENCE 190 AA; 21438 WW; 81BD4A7A.
STRAIN-ATCC 25586;
MEDLINE-21886394; PubMed-11889109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE010470; AAL93738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein AQ_755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002661; RRF. Pfam; PF01765; RRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 36.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus.
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01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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and for commercial
          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLATE CONTROL 13:611-619(1997).

-1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABOUND THE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PRE INDUCES AN ARRAY OF WORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PRE CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Homodimer (By similarity).
-!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-|- SIMILARITY: Contains 2 PAS (PER-ARMY-SIM) dimerization domains.
-!- SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor (Sorghum) (Sorghum vulgare).

Subaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H., Morgan P.W., Mullet J.E.; The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alba R., Kelmenson P.W., Cordonnier-Pratt M.-M., Pratt L.H.; "The phytochrome gene family in tomato and the rapid differential evolution of this family in angiosperms."; Mol. Biol. Evol. 17:362-373(2000).
                                                                                                                                                      1;
                                                                                                                       29.5%; Score 52.5; DB 1; Length 242; 45.8%; Pred. No. 9.2;
                                                                                                                                                    5; Indels
δq
                                                                    PIR; B70366; B70366.
Hypothetical protein; Complete proteome.
SEQUENCE 242 AA; 28618 MW; CE2C25680D721E93 CRC64;
 Usage
                                                                                                                                                                                                                                                                                                         (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                PRT; 1178 AA
                                                                                                                                                    7; Mismatches
                                                                                                                                                                                10 HRERSLQT-LRDIQRMLFPDEKEF 32
                                                                                                                                                                                                            60 HKRTSLRKFVREIEKMVFEAEKEF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. 58M;
MEDLINE=20188796; Pubmed=10723737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97198556; PubMed=9046599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 208-1178 FROM N.A.
                                                     EMBL; AE000706; AAC06923.1; -.
                                                                                                                   Query Match
Best Local Similarity 45.89
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phytochrome B.";
                                                                                                                                                                                                                                                                                                                                                                                                                         PACCAD clade; Pa
NCBL_TaxID=4558;
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                                                                                                                                                                                                                                                                                                                                                        Phytochrome B
                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                        28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                  PHYB OR MA3
                                                                                                                                                                                                                                                                                   PHYB_SORBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sudimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52.5;
send an email to license@isb-sib.ch).
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SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASe_c; 1.
SMART; SM00388; HisKa; 1.
SMART; SM00091; PAS; 2.
TIGREAMS; TIGR00229; SEDSOTY_DOX; 2.
                                                                       InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS5012; PAS; 2.
PROSITE; PS00245; PHYTOCHROME 1; 1.
PROSITE; PS50046; PHYTOCHROME 2; 1.
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MEDLINE-93054341; PubMed=1385387;
                                                                                                                       InterPro; IPR003661; His_kinA.
InterPro; IPR005467; His_kinase.
InterPro; IPR001014; PAS_domain.
InterPro; IPR001294; Phytochrome
Pfam; PF01590; GAF; 1.
Pf02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
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(Rel. 28, Last seq
                                                                                                                                                                                                                                                                              Pfam; PF00512; HisKA; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA polymerase sigma-B factor. SIGB OR ALL7615.
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                                                     EMBL; AF182394; AAB41398.2;
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DOMAIN 668 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pcc7120alpha
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28-FEB-2003
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FIT Cyanobacterium Anabaena sp. strain PCC 7120.";

KIE, DAN Res. 88 205-213(2001).

- 1- FUNCTION: THE SIGNA FACTOR IS AN INITIATION FACTOR THAT PROMOTES

CT ATTACHEMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND

THEN IS RELEASED.

- 1- SIMILARITY: Belongs to the sigma-70 factor family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration of the European Bioinformatics and the EMBL outstation of the European Bioinformatics and the EMBL outstation of the European Bioinformatics and the EMBL outstation of the European Bioinformatics as incent is in no way conditied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/cc rend an email to licensedish-sib.ch).

CC rend an email to licensedish-sib.ch).

DR EMBL; M95760; AAA22046.1; -.

DR EMBL; M95760; AAA22046.1; -.

DR Ffam; PF04519; Sigma-70.

BR PTR; AD241; AD2541.

DR PFAM; PF04545; Sigma-70.71.2; 1.

DR PFAM; PF04559; Sigma-70.71.2; 1.

DR PFAM; PF04559; Sigma-70.72; 1.

DR PFAM; PF04559; Sigma-70.72; 1.

DR PROSITE; PS00716; SIGMA70.2; 1.

PROMAIN 125 138 AM; B1323E670CCDP46A CRC64;

COMPAND 125 132 AA; SCORE 52; DB 1; Length 332;

Best Local Similarity 35:5; PS 17 Indels 0; Gaps 0;
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Search completed: October 15, 2003, 10:31:02 Job time : 6.22179 secs

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October 15, 2003, 10:27:33 ; Search time 20.2918 Seconds (without alignments) 445.097 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA 35
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Description	Q8z8y6 salmonella	Q8zre3 salmonella	Q9nt51 homo sapien	Q9y2h2 homo sapien	Q9vxu1 drosophila	Q9vxu2 drosophila	Q8uca0 agrobacteri	Q8d153 synechococc	Q8izm6 homo sapien	Q8tgz1 methanopyru	Q8vd56 rattus norv	014687 homo sapien	014686 homo sapien	067532 aquifex aeo	Q8prd9 xanthomonas	001302 caenorhabdi
a a	Q8Z8Y6	Q8ZRE3	Q9NT51	Q9Y2H2	Q9VXU1	09VXU2	QBUCAO	Q8DI53	Q812M6	Q8TGZ1	Q8VD56	014687	014686	067532	Q8PRD9	001302
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32.0%; Score 57; DB 16; Length 1034; 42.9%; Pred. No. 68;

Query Match Best Local Similarity

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Hypothetical protein.
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SEQUENCE
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MEDLINE-21534948; PubMed=11677609;
MCDLINE-21534948; PubMed=11677609;
MCDLINE-21534948; PubMed=11677609;
MCCLELland M., Sanderson K.E., Spieth J., Clifton S.W., Latrellle P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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EMBL; AL137528; CAB70792.1; -.
InterPro; IPR002013; Syja_N.
Pfam: PF02383; Syja_N:
PROSITE; P550275; SAC; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 16; Length 1046; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exonuclease; Complete proteome.
SEQUENCE 1046 AA: 117824 MW; BA565CA3BDAD0C82 CRC64;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
DKF2F434P1818.
                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      859 AA.
                                                                                                                                                                                                                                                                                    PRT; 1046 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 LADEQLQQLEASLQALTDEEKRLLADQQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LSQEQLEHRERSLQTLRDIQRMLFPDEK 30
                                                             3 LSQEQLEHRERSLQTLRDIQRMLFPDEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).

EMBL; AE008713; AAL119349.1; -.

InterPro; IPR004319; ABC_transporter.

InterPro; IPR004592; SbC_.

InterPro; IPR004395; SMC_.N.
                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Last 01-MAR-2003 (TrEMBLrel. 23, Last ATP-dependent dsDNA exonuclease.
      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02463; SMC_N; 1.
TIGRFAMS; TIGR00618; sbcc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.0%;
42.9%;
                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.0 Best Local Similarity 42.9 Matches 12; Conservative
   Conservative
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECC OR STM0395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
   12;
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                                                                                                                                                                                                                                                                                    Q8ZRE3
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Q9NT51
      Matches
                                                                                                                                                                                                                   RESULT 2
QBZRE3
1D QBZRE3
AC QBZRE3
DT 01-M
DE ATP-
COX BACL
COX BA
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Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                                                                        Gaps
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    ;
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01-OCT-2002 (TIEMBLrel. 22, Last sequence update)
01-OCT-2002 (TIEMBLrel. 23, Last annotation update)
01-MAR-2003 (TIEMBLrel. 23, Last annotation update)
0332587 protein.
0G32587 OR CG6350 OR CG7821.
Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Neopters, Endoptersygota, Dipters, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
31.5%; Score 56; DB 4; Length 1132;
Best Local Similarity 33.3%; Pred. No. 1e+02;
Matches 10; Conservative 8; Mismatches 12; Indels
                                                                                       DB 4; Length 859; 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128407 MW; 853719FC0AD455CD CRC64;
1
96781 MW; BCBBC47C8B726D76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Hypothetical protein KIAA0966.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1132 AA.
                                                                                                                                                                                                                                                  5 QEQLEHRERSLOTLRDIQRMLFPDEKEFTG 34
                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                               5 QEQLEHRERSLQTLRDIQRMLFPDEKEFTG 34
                                                                                       31.5%; Score 56; 33.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002013; Syja_N.
Pfam; PF02383; Syja_N; 1.
PROSITE; PS50275; SAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB023183; BAA76810.1;
                                                                             Query Match
Best Local Similarity 33.33
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Ballew R.M., Basu A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barendale J., Brokatein P., Boldbakov S.,
RA Beeson K.Y., Busman D.A., Burler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busman D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Berriers S., Pleischmann W.,
RA Dourbin K.J. Evangelista C.C., Ferriers S., Pleischmann W.,
RA Barris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA dlodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Aluston N., Havyey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Almanl B.E., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Minnell B.E., Kadira C.D., Kraft C., Kravitz S., Wolp D. L.,
RA Alusko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Markulov G., Milshina N.V., Mobarty C., Morris J.N. Nosherson D.L.
RA Palazzolo M., Pittama G.S., Pan S., Pollard J., Puri V., Rese M.G.,
RA Reinert K., Remington K., Saunders R., Varion B.C., Scheeler F., Shen H.,
RA Spier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B.C., Suden-Kiamos I., Simpson M., Skupski M.P., Smith H.O.,
RA Williams S.M., Woodage T., Worlex E., Wang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worlex E., Wang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worlex E., Wang S., Yao Q.A.,
RA Gibbs R.A., Merre E.W., Rubin G.M., Venter J.C.;
R. Schence 287:2185-2195(2000).
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R. Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J.B., Busam D.A.,
Carlson J.W., Center A. Davenport L.B., Dietz S.M.,
Carlson J.W., Center A. Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
R. Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
R. McIntosh T.C., Moy M., Murphy B., Nelson C., Telffer B., Rocheler F.,
R. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman E., Garlson J.W., Celniker S.E., Kichmiller D., Prise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE003499; AAF48467.2; -. FlyBase; FBGN05587; CZPS 137774 MW; 131F2EB663826A92 CRC64; SEQUENCE 1208 AA. 137774 MW;

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ESQUENCE FROM N.A.

RESQUENCE FROM N.A.

RESQUENCE FROM N.A.

RA AMABELINE-20196006; PubMed-10731132;

RA AMABELINE-20196006; PubMed-10731132;

RA AMABELINE-20196006; PubMed-10731132;

RA AMABELINE-20196006; PubMed-10731132;

RA AMABELINE-2019606; Schere S.E., Richards S., Ashburner M., Henderson S.N., Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix,

RA Brandon R.C., Rogers T.H.C., Blazel R.G., Champe M., Pfelifer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helf G., Champe M., Pfelifer B.D.,

RA Abril J.F., Agbayani A., Helf G., Relson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cosler C., Gabrielian A.E., Garg N.S., S., Reriacs S., Ferischman W.,

RA Doubin K.J., Evangelista C.C., Perrac C., Ferriers S., Ferischman R.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Astris N.L., Harvey D., Belman T.J., Hernandez J.R., Houston K.A., Howland T.J., Well M.-H., Ibeyam C.,

RA Astris N., Marvey D., Reiman T.J., Well M.-H., Ibeyam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milbina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milbina N.V., Mobarry C., Morris J., Pusher S., Pacleb J.M.,

RA Merkulov G., Milbina N.V., Mobarry C., Wursher M., Shron B., Shith T.,

RA Reinert K., Femington K., Saunders R., Verlons, S., Yao, O. A.,

RA Mang Z., Teccor C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-, Y., Wassarman D.A., Wellson D., Wullians S., Willians S., Willians S., Willians S., Willians S., Willians S.,
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                                                       Gaps
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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
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                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
0632587 protein (SD07366p).
0632587 OR CG6550 OR CG7851.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Phydroidea; Drosophilidae; Drosophila.
  Length 1208;
Score 56; LL = ...
Pred. No. 1.1e+02;
31.5%; Score 56; DB 5; 45.5%; Pred. No. 1.1e+02
                                                                                                                                                                                                                                                                                  PRT; 1398 AA.
                                                  6; Mismatches
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811 LQQQAESQEQQASTLRDLERL 832
                                                                                                    3 LSQEQLEHRERSLQTLRDIQRM 24
Query Match 31.55
Best Local Similarity 45.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                            Q9VXU2; Q960D0;
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Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
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Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
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Sequencing of Drosophila melanogaster genome. ".
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky D., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Annotation of Drosophila melanogaster genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1 ranscriptional regulator, RpiR family.
4 Transcribt tunefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Matches 10; Conservative
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Caot V. Askenazi M., Halling C., Mullin L.,
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                                                                                           The genome of the natural genetic engineer Agrobacterium tumefaciens
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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EMBL; AP005375; BAC09290.1; -
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Transfer RNA-Gin reductase.
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265 QQRQRSMVTLRHIKQQLVEHRDPDDKQLLG 294
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                                                                                                                                                            Science 294:2317-2323(2001).
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Matches 10; Conserv
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nes 12; Conserv
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134 GFSQTLLEKLERLLHELRDIDRVV 157
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SEQUENCE
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KEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-21927647; PubMed=11930014;

A Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Andlykh A.G., Koonin E.V., Kozyatkin S.A.;

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The complete genome of hyperthermophile Methanopyrus kandleri AV19

The mad monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

REMBL, AE010374; AAM2048-1;

REMBL, AE010374; AAM2048-1;

RITCEPPO; IPR001550; Helicase.

RITCEPPO; IPR001550; Helicase.

REMBL, PF00270; DEAD.

REMBL, PF00270; DEAD.

REMBL, PF00271; Helicase.

REMBL, PF00271; Helicase.

REMBL, PF00271; Helicase.
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                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shang X., Zhou Y.T., Low B.C.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF544240; AANA(0769.1; -
SEQUENCE 433 AA; 49691 MW; OAE4B42A404AEID3 CRC64;
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SEQUENCE 818 AA; 91715 MW; C2136200A710817E CRC64;
                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
1-WAR-2003 (TrEMBLrel. 23, Last annotation update)
BCH domain-containing CdC42GAP-like protein.
BPGAPI
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Archeea-specific superfamily II helicase.
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                                                                    433 AA.
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SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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Best Local Similarity 54.25
Matches 13; Conservative
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GLSQEQLEHRERSLQTLRDIQRML 25

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"Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila trithorax.";
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                   Yoshida S., Ohbo K., Takakura A., Takebayashi H., Okada T., Abe K.,
Nabeshima Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97388474; PubMed=9247308;
Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 AA; 18146 MW; 6EBABD1DA16B88D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Putative bHLH transcription factor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 53.5; DB
; Pred. No. 28;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4957 AA
155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 15:549-560(1997).
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
EMBL; AF010404; AAC51735.1;
Interpro; IPR003889; FYI:ch_C.
InterPro; IPR003888; FYI:ch_N.
InterPro; IPR000910; HMG_12_box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                  Created)
 PRT;
                                                                                                                                                                                                                    STRAIN-Sprague-Dawley;
MEDLINE-21643927; PubMed*11784080;
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05,
23,
                               01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
PRELIMINARY;
                                                                                                                   Rattus norvegicus (Rat)
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5262 AA; 564171 MW; 26B7C74CAD417E44 CRC64;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T., Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                             30.1%; Score 53.5; DB 4; Length 4957; 42.5%; Pred. No. 9.6e+02; Live 4; Mismatches 12; Indels 7;
                                                                                                                                                                                                                                   SMART; SMUUJUU, ...
SMART; SMUUJUU, SET; 1.
SMART; SMO0317; SET; 1.
PROSITE; PS5001898; SET; 1.
PROSITE; PS50016; ZF_PHD_2; 1.
PROSITE; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2091 GLSQTELE-KQRQRQRLRELLIRQQIQRNTLRQEKETAAA 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GLSQEQLEHRERSLQTLRD----IQRMLFPDEKEFTGA
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-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
EMBL; AF010403; AAC51734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00508; POSTSET; 1.
SMART; SM00184; RING; 3.
SMART: SW00317; SET; 1.
PROSITE; PS00398; RECOMBINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC: 173; MLL2.
InterPro; IRR003889; FYrich_C.
InterPro; IRR003889; FYrich_C.
InterPro; IRR003889; FYrich_M.
InterPro; IRR006116; HMG_12_box.
InterPro; IRR006118; Recombinase.
InterPro; IRR00114; SET.
InterPro; IRR00114; SET.
InterPro; IRR001805; Znf_PHD.
InterPro; IRR001801; Znf_ring.
Ffam; PR00856; SET; 1.
SMART; SM00542; FYRC; 1.
SMART; SM00542; FYRC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=97388474; PubMed=9247308;
                        Recombinase.
                                                               Interpro: IPR001965; Znf_PHD.
Pfam: PF00628; PHD: 3.
Pfam: PF00856; SET: 1.
SMART: SM00542; FYRC: 1.
SMART: SM00541; FYRN: 1.
SMART: SM00249; PHD: 4.
SMART: SM00249; PHD: 4.
SMART: SM00249; PHD: 4.
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PS50016; ZF_PHD_2; 1.
PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 42.5%;
Matches 17; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00398; HMG; 1.
SMART; SM00249; PHD; 7.
                                                IPR001214; SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                          InterPro;
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1014686

AC 014688

AC 01468

DT 01-JA DT

O1-JA DT

O1-JA DT

O1-JA DLR.

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CSTRAIN-306 / ATCC 13902 / XV 101;

CM MEDLINE-21022145; PubMed=1202421;

CM ADLINE-21022145; PubMed=1202421;

CM ADLINE-21022145; PubMed=1202421;

CM ADLINE-21032145; PubMed=1202421;

CM CHARLO J.A. Relnach F.C., Farah C.S., Furlan L.R.,

CM CHARLO J. M.C., Canavan J.E.,

CM Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

CM Clarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

CHARLO J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

COMMISSION M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

CALOGALIE C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meldanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Garham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                               7;
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        DB 4; Length 5262;
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                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 392:353-358(1998).
EMBL, AE000747. AACO7503.1, -.
Hypothetical protein; Complete proteome.
SEQUENCE 227 AA; 27375 MW; 3F9E80A29D606B61 CRC64;
                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC0024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein AQ_1596.
                                                                                                                                                              2 GLSQEQLEHRERSLQTLRD-----IQRMLFPDEKEFTGA
30.1%; Score 53.5; DB 42.5%; Pred. No. 1e+03; ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                227 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                         Best Local Similarity 42.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=92829;
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    Query Match
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067532
ID 067532
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Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Srindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitalima J.P., "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."

EMBL; ABO11625, AAM34916.1; --
EMBL; ABO11625, AAM34916.1; --
EMBL; APO11625, Peptidase_M37.

Pfam; PF01551; Peptidase_M37.

Hypothetical protein; Complete proteome.

SEQUENCE 411 AA; 44337 MW; E193496126355426 CRC64;
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                    Query Match

29.8%; Score 53; DB 16; Length 411;
Best Local Similarity 36.4%; Pred. No. 89;
Matches 12; Conservative 4; Mismatches 17; Indels
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Search completed: October 15, 2003, 10:35:47 Job time: 23.2918 secs